

PA (INSP) INST PASTEUR.
PA (INRM) INST NAT SANTE & RECH MEDICALE.
PI Benarous R, Margottin F, Durand H, Arenzana Seisdedos F, Kroll M,
PI Concorde J;
DR MPI; 1999-469329/39.
DR N-PSDB; AAX86501.
PT New human beta-tranaducin repeat containing protein and its fragments
PT useful as, or to screen for, antiviral, antitumor, anti-inflammatory and
PT anti-Alzheimer agents.
PS Claim 1, Page 60-61; 71pp; French.
XX
XX The present sequence represents a human beta-tranaducin repeat containing
CC protein (beta-Trip). The protein directs proteins to the proteosome
CC degradation pathways. The protein is able to interact with the Vpu
CC protein of human immune deficiency virus-1 (HIV-1), cellular proteins
CC IkappaB or beta-catenin (bc) and/or protein Skp1. The protein controls
CC ubiquitinylation of phosphorylated proteins and thus their targeting to
CC proteosomes for degradation. Depending on whether the process is
CC inhibited or promoted, the result may be delayed breakdown of CD4 (in
CC cases of HIV-1 infection); increased activity of Ikb (and thus reduced
CC activity of NFkappaB) and increased degradation of mutant bc in tumour
CC cells, or increased bc survival (and reduced apoptosis) in Alzheimer's
CC patients. The beta-Trip protein, and its active peptide fragments, or its
CC nucleic acid, are used to screen for anti HIV-1 agents (antivirals),
CC antitumour agents that disrupt cell cycle regulation or protein
CC degradation in human tumour cells, and anti-inflammatory agents that
CC disrupt activation by NFkappaB. Fragments of the protein are also useful
CC for treating osteo-articular inflammation or acute inflammation
CC associated with release of tumour necrosis factor. (Updated on 20-MAR-
CC 2003 to correct PA field.)
XX
XX Sequence 569 AA;
SQ
Query Match 100.0%; Score 3034; DB 2; Length 569;
Best Local Similarity 100.0%; Pred. No. 7,4e-286;
Matches 569; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MDPAAVLQEKALKFMSNSEREDCNNGEPKRIPEKNSLRQTYNSCARLCINQETVCLA 60
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DB 61 STAMTENCVAKTLANGTSSMTIVPKOKLASYEKEKELCYKYEQMSSESQVFEVHL 120
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DB 121 ISOMCHYOHGHINSYLPKMLQRPFTALPARGLDIAENILSYLAKSLCAAEVCKEEM 180
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DB 181 RVTSDGMLWKLLIERMVRTDSLMRGLAERRGQYLFKNKPPDGNAPPSFYRALYPKII 240
QY 241 ODIEFTESNMRCGRSLQRIHCRSETSKGVYCLQYDDQKISGLADNTIKIMDKTLECK 300
DB 241 ODIEFTESNMRCGRSLQRIHCRSETSKGVYCLQYDDQKISGLADNTIKIMDKTLECK 300
QY 301 RLITGHTSSVLCLOYDERVIITGSSDSYTVRVMDVNTGEMLNTLIHHCEAVLHLRFNNGMM 360
DB 301 RLITGHTSSVLCLOYDERVIITGSSDSYTVRVMDVNTGEMLNTLIHHCEAVLHLRFNNGMM 360
QY 361 VTCSKORSIAVWDMASPTDITLRLVVGHRAAVNVVDPDDKXIVASAGDRITIKWNTSTC 420
DB 361 VTCSKORSIAVWDMASPTDITLRLVVGHRAAVNVVDPDDKXIVASAGDRITIKWNTSTC 420
QY 421 EHVRLTLNGHKRIACIQYRDLRVVSGSSPNTRLMDIEGACLRVLEGHEELVRCIRPDN 480
DB 421 EHVRLTLNGHKRIACIQYRDLRVVSGSSPNTRLMDIEGACLRVLEGHEELVRCIRPDN 480

QY 481 KRIVGAYDGKIKWMDLVAAIDPPAPAGTLCRLTLVHSGRVFLQDFEQIVSSSHDDT 540
DB 481 KRIVGAYDGKIKWMDLVAAIDPPAPAGTLCRLTLVHSGRVFLQDFEQIVSSSHDDT 540
QY 541 ILIWDPLNDPAAQEPSPSPRTTYISR 569
DB 541 ILIWDPLNDPAAQEPSPSPRTTYISR 569
RESULT 2
AAV44249
ID AAV44249 standard; protein; 569 AA.
XX
XX AAV44249;
AC
XX
DT 28-FEB-2000 (first entry)
XX
XX Human cell signalling protein-12.
DE
XX Cell signalling protein-12; CSIGP-12; cell proliferation;
KW inflammatory disorder; cirrhosis; cancer; hepatitis; AIDS;
KW arteriosclerosis; Addison's disease; multiple sclerosis.
XX Homo sapiens.
XX
XX
XX Key
FT Modified-site
FT /note= "Potential glycosylation site"
FT 17
FT Modified-site
FT /note= "Potential phosphorylation site"
FT 19
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FT /note= "Potential phosphorylation site"
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FT /note= "Potential phosphorylation site"
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FT /note= "Potential phosphorylation site"
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FT /note= "Potential phosphorylation site"
FT 320, .334
FT Region
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FT 328
FT Modified-site
FT /note= "Potential phosphorylation site"
FT 360, .374
FT Region
FT /label= Signature_sequence
FT 376
FT Modified-site
FT /note= "Potential phosphorylation site"
FT 381
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FT /note= "Potential phosphorylation site"
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FT 416
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FT /note= "Potential glycosylation site"
FT 418
FT Modified-site
FT /note= "Potential phosphorylation site"
FT 443, .457
FT Region
FT /label= Signature_sequence
FT 451
FT Modified-site
FT /note= "Potential phosphorylation site"
FT 483, .497
FT Region
FT /label= Signature_sequence
FT 514
FT Modified-site
FT /note= "Potential phosphorylation site"
FT 519
FT Modified-site
FT /note= "Potential phosphorylation site"
FT 532, .546
FT Region

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FT      Modified-site      /label= Signature_sequence
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FT      /note= "Potential phosphorylation site"
FT      Modified-site      536
FT      /note= "Potential phosphorylation site"
XX      MO9958558-A2.
XX      18-NOV-1999.
XX      13-MAY-1999; 99WO-US010567.
XX      13-MAY-1998; 98US-0085343P.
XX      26-AUG-1998; 98US-0098010P.
XX      (INCY-) INCYTE PHARM INC.
XX      Bandman O, Hillman JL, Lal P, Yue H, Tang YT, Patterson C,
XX      Baughn MR, Yang J;
XX      WPI: 2000-086432/07.
XX      N-PSDB; AA229233.
XX      Human cell signaling proteins useful for, e.g. diagnosing cell
XX      proliferative and inflammatory disorders.
XX      Claim 1; Page 77-78; 90pp; English.
XX      The present sequence is cell signaling protein-12 (CSIGP-12) encoded by
XX      cDNA obtained from Incyte clone 3293149 of COLAUCT01 library. It is
XX      expressed in musculoskeletal, gastrointestinal and nervous tissues and is
XX      found to be homologous to beta-transducin repeats containing protein.
XX      Fragments of CSIGP encoding nucleic acid can be used as hybridisation
XX      probe for detecting CSIGP related sequences or allelic variants.
XX      Recombinant CSIGP can be produced in host cells by transforming them with
XX      genetically engineered vectors. Agonists or antagonists can be used in
XX      the treatment of cell proliferative and inflammatory disorders associated
XX      with decreased or increased CSIGP expression. CSIGP is used in the
XX      diagnosis, prevention and treatment of cell proliferative disorders like
XX      arteriosclerosis, cirrhosis, cancer, hepatitis and inflammatory disorders
XX      like AIDS, Addison's disease, multiple sclerosis, etc
XX      Sequence 569 AA;
SQ
Query Match      100.0%; Score 3034; DB 3; Length 569;
Best Local Similarity 100.0%; Pred. No. 7.4e-286;
Matches 569; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB      1 MDPAAVAVLOEKALKFMNSSEEDCNNGEPKRIIPKNSLRQTVNSCARLCINQETVCLA 60
QY      61 STAMKTECNVAKTKLANGTSSMIVPKQRKLSASYEKEKELCVKYPEQWSESQVEFVEHL 120
DB      61 STAMKTECNVAKTKLANGTSSMIVPKQRKLSASYEKEKELCVKYPEQWSESQVEFVEHL 120
QY      121 ISQMGCHYGHGHTINSYKPMLOQDFITLAPARGLDHTAENIISYLDKAKSICAAELVCKEWMY 180
DB      121 ISQMGCHYGHGHTINSYKPMLOQDFITLAPARGLDHTAENIISYLDKAKSICAAELVCKEWMY 180
QY      181 RYTSQGMMLKMLIERVVRTDSLWRGLAERBGQGVYFKKPPDGNAPPSFPRALYPKTI 240
DB      181 RYTSQGMMLKMLIERVVRTDSLWRGLAERBGQGVYFKKPPDGNAPPSFPRALYPKTI 240
QY      241 QDIETIESNMRGCRSHLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNITIKIMDKNTLECK 300
DB      241 QDIETIESNMRGCRSHLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNITIKIMDKNTLECK 300
QY      301 RILTGHGTSVLCLODERVIYITGSSSDYTRVWDVNTGEMLNTLIHHCNAVHLRFRNGMM 360
DB      301 RILTGHGTSVLCLODERVIYITGSSSDYTRVWDVNTGEMLNTLIHHCNAVHLRFRNGMM 360
QY      361 VTCSKDRSIAVWDMASPTDITLRVYLVGRAAVNVVDPDKYIVASGDRITIKWNTSTNC 420

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DB      361 VTCSKDRSIAVWDMASPTDITLRVYLVGRAAVNVVDPDKYIVASGDRITIKWNTSTNC 420
QY      421 EFVRTLNHGKRGIACTQYRDRLVVSGSSDNTIRLMDIEGACRLVLEGHBEIVRCIRPN 480
DB      421 EFVRTLNHGKRGIACTQYRDRLVVSGSSDNTIRLMDIEGACRLVLEGHBEIVRCIRPN 480
QY      481 KRIVGAYDGTKIYKWDVLAALDPRAPAGTLCRLTVESHGVRVLOPQFQVSSSHDT 540
DB      481 KRIVGAYDGTKIYKWDVLAALDPRAPAGTLCRLTVESHGVRVLOPQFQVSSSHDT 540
QY      541 ILIWDPLNDPAAQAEPSPSRRTYTYISR 569
DB      541 ILIWDPLNDPAAQAEPSPSRRTYTYISR 569
RESULT 3
AA12813
ID      AA12813 standard; protein; 569 AA.
XX      AA12813;
XX      27-NOV-2000 (first entry)
XX      Human beta-transducin repeat containing protein (beta-Trcp) SEQ ID NO:3.
XX      Ubiquitin ligase SCF complex; F-box protein; ubiquitination; IkappaB;
XX      beta-catenin; Skp1; Cull; F-box motif; WD40 repeat motif; FWD1;
XX      gene therapy; colon cancer; beta-transducin repeat containing protein;
XX      beta-Trcp.
XX      Homo sapiens.
XX      JP2000166542-A.
XX      20-JUN-2000.
XX      02-DEC-1998; 98JP-00343437.
XX      02-DEC-1998; 98JP-00343437.
XX      (KAGA-) KAGAKU GIUTSU SHINKO JIGYODAN.
XX      WPI: 2000-485550/43.
XX      N-PSDB; AAA73132.
XX      F-box protein of ubiquitin ligase SCF complex which promotes the
XX      ubiquitination of IkappaB or beta-catenin.
XX      Claim 3; Page 10-12; 19pp; Japanese.
XX      The present invention describes an F-box motif protein of ubiquitin
XX      ligase SCF complex which promotes the ubiquitination of IkappaB or beta-
XX      catenin and is constituted by Skp1 protein, Cull protein and a complex
XX      (SCF complex) of F-box protein containing F-box motif and WD40 repeat
XX      motif and has the amino acid sequence of 45 residues (AA12811) or one of
XX      two 569 residue sequences (AA12812, which is mouse ubiquitin ligase FWD1
XX      protein) and (AA12813, which is human beta-transducin repeat containing
XX      protein (beta-Trcp)). The F-box protein can be used for the gene therapy
XX      of colon cancer by being recombined to a virus vector
XX      Sequence 569 AA;
SQ
Query Match      100.0%; Score 3034; DB 3; Length 569;
Best Local Similarity 100.0%; Pred. No. 7.4e-286;
Matches 569; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB      1 MDPAAVAVLOEKALKFMNSSEEDCNNGEPKRIIPKNSLRQTVNSCARLCINQETVCLA 60
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Db 121 ISOMCHYOHGHINSYTLKPMLOQDPFTLALPARGLDHAENIISYLDASLSLCAAEIVCKEMW 180
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QY 541 ILIMDFLNDPAAQAEPSPSPRTTYISR 569
Db 541 ILIMDFLNDPAAQAEPSPSPRTTYISR 569

RESULT 4

AA96697
ID AAY96697 standard; protein; 569 AA.

AC AAY96697;

DT 26-SEP-2000 (first entry)

DE Human beta-TTCP.

KK E3 ubiquitin ligase; beta-TTCP; F-box; WD protein; I-kappa-B; inhibitor;
KM nuclear factor kappa-B; NF-kappa-B; degradation; modulator; anti-viral;
KW anti-inflammatory; immunosuppressive; cyostatic.

XX Homo sapiens.

OS WO200034447-A2.

PN 15-JUN-2000.

PD 09-DEC-1999; 99WO-US029371.

PF 10-DEC-1998; 98US-00210060.

PR (SIGN-) SIGNAL PHARM INC.

PA (YISS) YISSUM RES & DEV CO.

PI Manning AM, Mercurio F, Amit S, Ben-Neriah Y, Davis M,

PL Hatzuda A, Lavon I, Yaron A;

DR WPI; 2000-431294/37.

DR N-PSDB; AAA51229.

PT Polypeptide enhancing phosphorylated I-kappa-B ubiquitination useful for
PT treating disorder associated with NF-kappa-B activation e.g. cancer,
PT comprising amino acid sequence of human E3 ubiquitin ligase or its
PT variant.

PS Claim 21; Page 72-74; 77pp; English.

CC Human beta-TTCP, an F-box/WD protein family member, has been shown to
CC have homology to human E3 ubiquitin ligase (E3). E3 enhances
CC ubiquitination of phosphorylated I-kappa-B, an inhibitor protein of
CC nuclear factor kappa-B (NF-kappa-B). Understanding I-kappa-B degradation
CC via the ubiquitin pathway is useful for identifying modulators of this
CC process for use in treating diseases associated with activation of NF-
CC kappa-B. In vitro analysis suggests that deletion of the F-box results in
CC a protein that functions as a dominant negative molecule in vivo.
CC Transient over-expression of delta-beta-TTCP (a deletion mutant)
CC inhibited the degradation of endogenous I-kappa-B-alpha in stimulated
CC Jurkat cells, resulting in accumulation of phosphorylated I-kappa-B-
CC alpha. E3 can be used to screen for modulators of NF-kappa-B activity. E3
CC and beta-TTCP can be used to modulate NF-kappa-B to treat inflammatory
CC diseases, autoimmune diseases, cancer and viral infections

XX Sequence 569 AA;

SQ Query Match 100.0%; Score 3034; DB 3; Length 569;

Best local Similarity 100.0%; Pred. No. 7.4e-286; Mismatches 0; Gaps 0;

Matches 569; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPAAVLQEKALKFNNSSEREDCNNGEPKRIIPKNSLRQTYNSCARLCLNGETVCLA 60

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Db 61 STAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEKELCVKPEQMSSEDOVEFEVHL 120

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Db 121 ISOMCHYOHGHINSYTLKPMLOQDPFTLALPARGLDHAENIISYLDASLSLCAAEIVCKEMW 180

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Db 181 RVTSDGMLMKKLIBRMVRTDLSMRGLAERRMGQYLFKNKPPDGNAPNSFYRALYPKII 240

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Db 241 ODIEETIESNMRCGRHSIORIHCRSETSKGVYCLQYDDOKIVSGLRDNTIKIMDKNTLECK 300

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Db 301 RILGHTGTSVCLQYDERVITITGSSDSIVRVWDVNTGEMNTLHHCBAVLHLRPNNGMM 360

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Db 361 VTCSKDRSIAVWDMASPTDITLRLRVLVGHRAAVNVVDFDDKXIVSASGDRITKWNSTGC 420

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Db 421 EFPVRLNGHKRGIACTQYRDRRLVVGSSSDNTIRLMDIECGACLRVLBGHEBLVRCIRPDN 480

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Db 481 KRIVSGAYDGKIKWMDLVAAALDPPAPAGTLCIRTIVHSGRVRLOPDEFOIVSSSHDT 540

QY 541 ILIMDFLNDPAAQAEPSPSPRTTYISR 569

Db 541 ILIMDFLNDPAAQAEPSPSPRTTYISR 569

RESULT 5

AA983250
ID AAY83250 standard; protein; 569 AA.

AC AAY83250;

DT 16-AUG-2000 (first entry)

DE F-box protein hbetatTcP.

XX Ubiquitin ligase; SCF; F-box protein; targeted degradation;
 KW destabilization; proteolysis; drug discovery; gene therapy; cancer;
 KW oncoprotein; Huntington's disease; gene knockout; delivery systems;
 KW human.
 XX Homo sapiens.
 OS
 XX MO200022110-A2.
 PN
 XX 20-APR-2000.
 PD
 XX 08-OCT-1999; 99WO-US023705.
 PF
 XX 09-OCT-1998; 98US-0103787P.
 PR
 XX (HARD) HARVARD COLLEGE.
 PA
 XX Zhou P, Howley P;
 PI
 XX WPI: 2000-317970/27.
 DR
 XX N-PSDB; AA293710.
 XX
 PT Targeting degradation of polypeptide useful for treating cancer and other
 PT proliferative disorders, involves conjugating polypeptide with ubiquitin
 PT protein ligase or inhibiting ubiquitination using organic compound.
 XX
 PS Claim 9, Page 171, 185pp; English.
 CC The F-box proteins are a family of ubiquitin ligases (SCF ubiquitin
 CC ligases) which can be used for the targeted degradation of a target
 CC polypeptide in vivo. Targeted degradation is achieved by expressing the
 CC ubiquitin ligase in a cell linked to the interaction domain of the target
 CC polypeptide and thereby recruiting the target polypeptide to the
 CC ubiquitin ligase. Such methods are useful for decreasing or increasing
 CC the level of a target polypeptide and for creating and expressing a
 CC destabilized polypeptide which is subjected to SCF mediated proteolysis.
 CC degrading any desired protein in a cell is useful for preventing or
 CC treating diseases caused by the presence of abnormal amount of the
 CC specific polypeptides, for drug discovery and for gene therapy. Diseases
 CC treated include cancer, by degradation of oncoproteins, Huntington's
 CC disease, other proliferative disorders and microbial infections. The
 CC method provides a quick and easy alternative to gene knockout technology.
 CC The target polypeptide can be degraded at all stages, or a specific
 CC stage, of development in the mature animal.
 XX
 XX Sequence 569 AA;
 SQ

Query Match 100.0%; Score 3034; DB 3; Length 569;
 Best Local Similarity 100.0%; Pred. No. 7,4e-286;
 Matches 569; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPAAVLQEKALFKPNSSERDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLA 60
 DB 1 MDPAAVLQEKALFKPNSSERDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLA 60
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 DB 61 STAMTEENCVAATKTLANGSSMTIVPKORLSASVEKEKELCKRYEQWSESQVFEVETL 120
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 DB 121 ISOMCHYGHGHSINSLKPMLODFITLALPARGLDIAENILSYLDAKSLCAELVCKEY 180
 QY 181 RYTSQGMILMKKLIERNVRTDSLWRGLAERGGQYLFKNKPPDGNAPNSFYRALYPKII 240
 DB 181 RYTSQGMILMKKLIERNVRTDSLWRGLAERGGQYLFKNKPPDGNAPNSFYRALYPKII 240
 QY 241 ODIEETESNMRGSRSLORIHCRSETSKGVYCLQYDDQKIVSGLANNTIKIMDKNTLREK 300
 DB 241 ODIEETESNMRGSRSLORIHCRSETSKGVYCLQYDDQKIVSGLANNTIKIMDKNTLREK 300
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DB 301 RILNHTGTSVLCIQYDERVILITGSSDSTVRVMDVNTGEMLNTLIHCEAVLHLRFNNGWM 360
 QY 361 VTCSKDRSLAVWDMASPDITLRLVVGHRRAVNVVDFPDKIVASGRRITKWNVTSTC 420
 DB 361 VTCSKDRSLAVWDMASPDITLRLVVGHRRAVNVVDFPDKIVASGRRITKWNVTSTC 420
 QY 421 EFRVTLNGHKRGIACTQYDRDLVWSSSDNTLRMDIEGACLRVLEGHEELVRCIRFDN 480
 DB 421 EFRVTLNGHKRGIACTQYDRDLVWSSSDNTLRMDIEGACLRVLEGHEELVRCIRFDN 480
 QY 481 KRIVSGAYDGKIKWMDLVAAALDPRAAPAGTLCLRTLVHSGRVRLQDFEQIVSSSHDT 540
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 QY 541 IILWDFLNDPAAQAEPSPSRRTTYISR 569
 DB 541 IILWDFLNDPAAQAEPSPSRRTTYISR 569

RESULT 6
 ID AAY83041 standard; protein; 569 AA.
 AC AAY83041;
 DT 16-AUG-2000 (first entry)
 DE F-box protein FBP-1.
 KW F-box protein; FBP; diagnosis; treatment; screening; agonist; antagonist;
 KW proliferative disorder; differentiative disorder; breast cancer;
 KW prostate cancer; ovarian cancer; cancer; small cell lung carcinoma;
 KW immune disorder; cardiovascular disorder; inflammatory disorder; human.
 OS Homo sapiens.
 PN MO200012679-A1.
 PD 09-MAR-2000.
 PF 27-AUG-1999; 99WO-US019560.
 PR 28-AUG-1998; 98US-0098355P.
 PR 03-FEB-1999; 99US-0118568P.
 PR 15-MAR-1999; 99US-012449P.
 PA (UYNV) UNIV NEW YORK STATE.
 PI Chitaur DS, Pagano M, Latres E;
 DR WPI: 2000-256635/22.
 DR N-PSDB; AA293350.
 PT Novel nucleic acid for screening compounds useful for treating
 PT proliferative and differentiative disorders such as cancer and immune
 PT disorders comprises sequences encoding ubiquitin ligases.
 PS Disclosure; Fig 3a; 245pp; English.
 XX Nucleic acids encoding substrate-targeting subunits of ubiquitin ligases
 CC with F-box motifs (F-box proteins) are useful for diagnosis of
 CC proliferative and differentiated related disorders by measuring FBP gene
 CC expression. Cells expressing such proteins or their fragments are useful
 CC for screening compounds. The compounds are agonists or antagonists, which
 CC are useful for treating a proliferative or differentiative disorder in a
 CC mammal such as breast, ovarian and prostate cancer and small cell lung
 CC carcinoma and also major opportunistic infections, immune disorders,
 CC cardiovascular diseases and inflammatory disorders. FBP protein, analogs,
 CC derivatives and their subsequences, anti-FBP antibodies are also useful
 CC in diagnosis of the disorders
 XX
 XX Sequence 569 AA;
 SQ

Query Match 100.0%; Score 3034; DB 3; Length 569;
 Best Local Similarity 100.0%; Pred. No. 7,4e-286;
 Matches 569; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MDPBAVLQEKALKFNNSSEREDCNGGPPPKIIPKNSLRQTNSCARLCLINQETVCLA 60
DB 1 MDPBAVLQEKALKFNNSSEREDCNGGPPPKIIPKNSLRQTNSCARLCLINQETVCLA 60
QY 61 STAMKTENCVAKTKLANGTSSMIVKQKRLASYPEKELCVKYPEQWSESQVEFVEHL 120
DB 61 STAMKTENCVAKTKLANGTSSMIVKQKRLASYPEKELCVKYPEQWSESQVEFVEHL 120
QY 121 ISOMCHYOHGHINSYLLKPMLOQDFITLAPARGLDHIENILSYLDASLCAAEIVCKEMY 180
DB 121 ISOMCHYOHGHINSYLLKPMLOQDFITLAPARGLDHIENILSYLDASLCAAEIVCKEMY 180
QY 181 RVTSDGMLMKKLIEMRWRTDSLMRGLAERGWGYLFPKNKPPDGNAPNPSFYRALYPKII 240
DB 181 RVTSDGMLMKKLIEMRWRTDSLMRGLAERGWGYLFPKNKPPDGNAPNPSFYRALYPKII 240
QY 241 QDIETIESNMRCGRHSLORIHCRSETSKGVYCLQYDDOKIVSGLDNTIKIWDKNTLECK 300
DB 241 QDIETIESNMRCGRHSLORIHCRSETSKGVYCLQYDDOKIVSGLDNTIKIWDKNTLECK 300
QY 301 RILTGHTGSVLCLOYDERVIITGSSDSTVRWVDVNTGEMLNTLIHCEAVLHLRPNNGMM 360
DB 301 RILTGHTGSVLCLOYDERVIITGSSDSTVRWVDVNTGEMLNTLIHCEAVLHLRPNNGMM 360
QY 361 VTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDPDKYIVASAGDRITIKWNTSTC 420
DB 361 VTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDPDKYIVASAGDRITIKWNTSTC 420
QY 421 EFWRLNGHKGKGIACLOQRDLVVGSSDNTIRLMDIECGALRYLGEHEELVRCIRPDN 480
DB 421 EFWRLNGHKGKGIACLOQRDLVVGSSDNTIRLMDIECGALRYLGEHEELVRCIRPDN 480
QY 481 KRIVGAYDGKIKVMDLVAALDPRAPAGTLCRLTVESGRRVLOPDEFOVSSSHDT 540
DB 481 KRIVGAYDGKIKVMDLVAALDPRAPAGTLCRLTVESGRRVLOPDEFOVSSSHDT 540
QY 541 ILIWDPLNDPAAQAEPSPRSRTTYIYSR 569
DB 541 ILIWDPLNDPAAQAEPSPRSRTTYIYSR 569

```

RESULT 7

ABG69473 standard; protein; 569 AA.

ABG69473;

21-OCT-2002 (first entry)

Human bait protein beta-Trcp1.

Human; yeast two-hybrid assay; adipocyte; bait protein; NIDDM;
 non-insulin diabetes mellitus; obesity; selected interacting domain; STD;
 protein-protein interaction map; PIM; anorectic; metabolic disorder.

Homo sapiens.

W0200253726-A2.

11-JUL-2002.

28-DEC-2001; 2001WO-EP015423.

02-JAN-2001; 2001US-0259377P.

(HYBR-) HYBRIGENICS.

PA (CNRS) CENT NAT RECH SCI.

XX

PI Legrain P, Marullo S, Jockers R;
 XX WPI; 2002-583612/62.
 DR N-PSDB; ABS51009.

PT Novel complex of protein-protein interactions in adipocyte cells for
 PT identifying compounds that modulate the protein-protein interactions and
 PT useful for treating obesity and metabolic disorders.

PS Claim 1; Page: 125pp; English.

The invention relates to a complex of protein-protein interactions
 (forming a protein-protein interaction map, PIM) in adipocyte cells as
 defined in the specification, or polynucleotides in adipocytes encoding
 for the polypeptides. Also included are a recombinant cell expressing the
 interacting polypeptides and a method of selecting a modulating compound
 in adipocyte cells, by cultivating a recombinant host cell on a selective
 medium containing a modulating compound and a reporter gene the
 expression of which is toxic for the recombinant host cell which is
 transformed with two vectors, where the first vector comprises a
 polynucleotide encoding a first hybrid polypeptide and DNA binding domain
 and the second vector comprising a polynucleotide encoding a second
 hybrid polypeptide and an activating domain that activates the toxic
 reporter gene, when the first and second hybrid polypeptides interact and
 selecting the modulating compound which inhibits the growth of the
 recombinant host cell (i.e. using the yeast two-hybrid system). The
 complexes are useful for identifying compounds that modulate the protein-
 protein interactions and useful for treating obesity and metabolic
 disorders e.g. non-insulin dependent diabetes mellitus, NIDDM. The
 compound isolated by the method is useful for treating and preventing of
 obesity or metabolic diseases. The interactions between the proteins of
 the complex further define a set of selected interacting domains, STD.
 The present sequence represents a member of the protein complex of the
 invention, used as the bait protein in the yeast two-hybrid assay. Note:
 The present sequence was not displayed in the specification but was
 obtained from its Genbank entry by the indexer

Sequence 569 AA;

Query Match 100.0%; Score 3034; DB 5; Length 569;
 Best Local Similarity 100.0%; Pred. No. 7,4e-286;
 Matches 569; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MDPBAVLQEKALKFNNSSEREDCNGGPPPKIIPKNSLRQTNSCARLCLINQETVCLA 60
DB 1 MDPBAVLQEKALKFNNSSEREDCNGGPPPKIIPKNSLRQTNSCARLCLINQETVCLA 60
QY 61 STAMKTENCVAKTKLANGTSSMIVKQKRLASYPEKELCVKYPEQWSESQVEFVEHL 120
DB 61 STAMKTENCVAKTKLANGTSSMIVKQKRLASYPEKELCVKYPEQWSESQVEFVEHL 120
QY 121 ISOMCHYOHGHINSYLLKPMLOQDFITLAPARGLDHIENILSYLDASLCAAEIVCKEMY 180
DB 121 ISOMCHYOHGHINSYLLKPMLOQDFITLAPARGLDHIENILSYLDASLCAAEIVCKEMY 180
QY 181 RVTSDGMLMKKLIEMRWRTDSLMRGLAERGWGYLFPKNKPPDGNAPNPSFYRALYPKII 240
DB 181 RVTSDGMLMKKLIEMRWRTDSLMRGLAERGWGYLFPKNKPPDGNAPNPSFYRALYPKII 240
QY 241 QDIETIESNMRCGRHSLORIHCRSETSKGVYCLQYDDOKIVSGLDNTIKIWDKNTLECK 300
DB 241 QDIETIESNMRCGRHSLORIHCRSETSKGVYCLQYDDOKIVSGLDNTIKIWDKNTLECK 300
QY 301 RILTGHTGSVLCLOYDERVIITGSSDSTVRWVDVNTGEMLNTLIHCEAVLHLRPNNGMM 360
DB 301 RILTGHTGSVLCLOYDERVIITGSSDSTVRWVDVNTGEMLNTLIHCEAVLHLRPNNGMM 360
QY 361 VTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDPDKYIVASAGDRITIKWNTSTC 420
DB 361 VTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDPDKYIVASAGDRITIKWNTSTC 420
QY 421 EFWRLNGHKGKGIACLOQRDLVVGSSDNTIRLMDIECGALRYLGEHEELVRCIRPDN 480
DB 421 EFWRLNGHKGKGIACLOQRDLVVGSSDNTIRLMDIECGALRYLGEHEELVRCIRPDN 480

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Db      421 EFVRTLNHGKRGIAQLQYRDRLVVGSSDNTIRLMDIECGACLRVLEGEHELVCIRFDN 480
QY      481 KRIVGAYDGKIKWMDLVAAALDPRAAGTLCRTLVESGVRFLQDFQIVSSSHDT 540
Db      481 KRIVGAYDGKIKWMDLVAAALDPRAAGTLCRTLVESGVRFLQDFQIVSSSHDT 540
QY      541 ILIWFNDPAAQAEPSPRSRTTYTISR 569
Db      541 ILIWFNDPAAQAEPSPRSRTTYTISR 569

RESULT 8
AAO22446
ID      AAO22446 standard; protein; 569 AA.
XX
AC      AAO22446;
XX
DT      11-OCT-2002 (first entry)
XX
DE      Human F-box protein FBP1 SEQ ID No 2.
XX
KW      Cytostatic; immunomodulator; cardiant; antiinflammatory; antimicrobial;
KW      proliferative; differentiative disorder; Skp2; F-box protein; cancer;
KW      ubiquitin ligase; breast cancer; prostate cancer; ovarian cancer;
KW      small cell lung carcinoma; immune disorder; parathyroid adenoma; FBP;
KW      inflammatory disorder; lymphoma; major opportunistic infection;
KW      certain cardiovascular disease; human.
XX
OS      Homo sapiens.
XX
PN      WO200255665-A2.
XX
PD      18-JUL-2002.
XX
PF      07-JAN-2002; 2002WO-US000311.
XX
PR      05-JAN-2001; 2001US-0260179P.
XX
PA      (UNIV ) UNIV NEW YORK STATE.
XX
PI      Pagano M;
XX
DR      WPI; 2002-599665/64.
XX
N-PSDB; AAL41041.
XX
PT      Screening compounds for treating proliferative disorders, e.g. breast
PT      cancer or prostate cancer, infections or immune disorders, comprises
PT      detecting a change in the activity of Skp2 with either p27 or Cks1.
XX
PS      Disclosure; Fig 3; 246pp; English.
XX
CC      The invention relates to screening compounds useful for the treatment of
CC      proliferative or differentiative disorders comprising detecting a change
CC      in the activity of Skp2 (F-box protein). The method is useful for
CC      screening compounds for the treatment of proliferative or differentiative
CC      disorders, particularly cancer. These compounds include small molecules,
CC      or compounds or derivatives or analogues of the new ubiquitin ligases.
CC      The compounds are useful for treating diseases such as cancer (e.g.
CC      breast cancer, prostate cancer or ovarian cancer, lymphoma, small cell
CC      lung carcinoma or parathyroid adenoma), major opportunistic infections,
CC      immune disorders, certain cardiovascular diseases or inflammatory
CC      disorders. This sequence represents an F-box protein (FBP) relating to
CC      the invention
XX
SQ      Sequence 569 AA;

Query Match      100.0%; Score 3034; DB 5; Length 569;
Best Local Similarity 100.0%; Pred. No. 7.4e-266;
Matches 569; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      61 STAKTENCVAKTKLANGTSSMIVPKORKLASAYEKELCVKYPEOWSESPOVEVEHL 120
Db      61 STAKTENCVAKTKLANGTSSMIVPKORKLASAYEKELCVKYPEOWSESPOVEVEHL 120
QY      121 ISOMCHYOHGHINSYLYKPMLODFITALPARGLDHIAENIISYLDKSLCAAEVCKEY 180
Db      121 ISOMCHYOHGHINSYLYKPMLODFITALPARGLDHIAENIISYLDKSLCAAEVCKEY 180
QY      181 RVTSDGMLMKKLIBRMVRTDSLWRGLAERGMGYLFXNKPDPGNAAPPNSFYRALYPKII 240
Db      181 RVTSDGMLMKKLIBRMVRTDSLWRGLAERGMGYLFXNKPDPGNAAPPNSFYRALYPKII 240
QY      241 ODIEETIESNRCGRSLQRIHCRSETSGVYCLQYDDQKIVSGLDNNTIKIWDKNTLECK 300
Db      241 ODIEETIESNRCGRSLQRIHCRSETSGVYCLQYDDQKIVSGLDNNTIKIWDKNTLECK 300
QY      301 RILTGHTGSVLCLOYDERVIIITGSSDSITVRVWDVNTGEMLNTLIHCEAVLHLRFNNGM 360
Db      301 RILTGHTGSVLCLOYDERVIIITGSSDSITVRVWDVNTGEMLNTLIHCEAVLHLRFNNGM 360
QY      361 VTCSKORSIAVDMASPTDITLRRVLVGHRAAVNVDPDKYIVASGDRITKWNSTC 420
Db      361 VTCSKORSIAVDMASPTDITLRRVLVGHRAAVNVDPDKYIVASGDRITKWNSTC 420
QY      421 EFVRTLNHGKRGIAQLQYRDRLVVGSSDNTIRLMDIECGACLRVLEGEHELVCIRFDN 480
Db      421 EFVRTLNHGKRGIAQLQYRDRLVVGSSDNTIRLMDIECGACLRVLEGEHELVCIRFDN 480
QY      481 KRIVGAYDGKIKWMDLVAAALDPRAAGTLCRTLVESGVRFLQDFQIVSSSHDT 540
Db      481 KRIVGAYDGKIKWMDLVAAALDPRAAGTLCRTLVESGVRFLQDFQIVSSSHDT 540
QY      541 ILIWFNDPAAQAEPSPRSRTTYTISR 569
Db      541 ILIWFNDPAAQAEPSPRSRTTYTISR 569

RESULT 9
ADS88273
ID      ADS88273 standard; protein; 569 AA.
XX
AC      ADS88273;
XX
DT      18-NOV-2004 (first entry)
XX
DE      Human protein of a TNF-alpha signalling pathway protein complex Seq 128.
XX
KW      protein complex; tumour necrosis factor-alpha signalling pathway;
KW      TNF-alpha; chronic inflammatory disease; rheumatoid arthritis;
KW      inflammatory bowel disease; infectious disease; septic shock;
KW      bacteremia; neurological disease; stroke-induced inflammation;
KW      neurodegenerative disease; cancer; antiinflammatory; antiarthritic;
KW      antirheumatic; cytostatic; antibacterial; gene therapy; human.
XX
OS      Homo sapiens.
XX
PN      WO2004035783-A2.
XX
PD      29-APR-2004.
XX
PF      24-SEP-2003; 2003WO-EP050655.
XX
PR      26-SEP-2002; 2002EP-00021809.
XX
PR      10-FEB-2003; 2003EP-00100274.
XX
PA      (CELL-) CELLZOME AG.
XX
PI      Boumester T, Hulse B, Bauch A, Ruffner H, Bauer A, Kuester B,
PI      Superti-Furga G, Kruse U;
XX
DR      WPI; 2004-348460/32.
XX

```


PT New protein complex comprising at least one first and second protein of
PT the Tumor Necrosis Factor-alpha (TNF-alpha)-signaling pathway, useful for
PT diagnosing or treating inflammation, neurological diseases, infectious
PT diseases or cancer.

XX Example; SEQ ID NO 128; 1980bp; English.

CC This invention relates to novel protein complexes of the tumour necrosis
CC factor-alpha (TNF-alpha) signalling pathway. Specifically, it refers to
CC methods for preparing these complexes comprising at least two component
CC proteins, as well as screening methods to identify modulators of the
CC pathway, which include antibodies, agonists and antagonists thereof. The
CC present invention describes a protein complex and kit that are useful for
CC diagnosing, prognosing or treating chronic inflammatory diseases such as
CC rheumatoid arthritis and inflammatory bowel disease; infectious diseases
CC such as septic shock and bacterial infections; neurological diseases such
CC as stroke-induced inflammation in neurons; neurodegenerative diseases and
CC cancer. Accordingly, these complexes can be used for the development of
CC pharmaceutical compositions that exhibit antiinflammatory, antiarthritic,
CC antirheumatic, cytostatic and antibacterial activities and can be used
CC for gene therapy purposes. In particular, the invention further provides
CC siRNA-oligonucleotides useful for inhibiting protein expression for in
CC vitro or cell culture assays. This polypeptide is a human protein that
CC can be used in combination with other proteins provided in the
CC specification to form novel complexes of the TNF-alpha signalling pathway
CC of the invention.

CC Sequence 569 AA;

Query Match 100.0%; Score 3034; DB 8; Length 569;
Best Local Similarity 100.0%; Pred. No. 7.4e-286;
Matches 569; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPAAVIOEALKKFNMSSEREDCNNGEPKRIPEKNSLRQTYNSCARCLCINOETVCLA 60
DB 1 MDPAAVIOEALKKFNMSSEREDCNNGEPKRIPEKNSLRQTYNSCARCLCINOETVCLA 60
QY 61 STAMKTENCVAKTKLANGTSSMIVPKORKLSASYEKEKELCVKYFEQMSBDOVEFEVHL 120
DB 61 STAMKTENCVAKTKLANGTSSMIVPKORKLSASYEKEKELCVKYFEQMSBDOVEFEVHL 120
QY 121 ISOMCHYOHGHINSYLYKPMLOQDFITLAPARGLDHIENILSYLDKSLCAAEIVCKEMY 180
DB 121 ISOMCHYOHGHINSYLYKPMLOQDFITLAPARGLDHIENILSYLDKSLCAAEIVCKEMY 180
QY 181 RYTSNGIMMKKLIEMVWRTDSIMRGLAERKGGYLLFKKPPDGNAPNSFYRALYPKII 240
DB 181 RYTSNGIMMKKLIEMVWRTDSIMRGLAERKGGYLLFKKPPDGNAPNSFYRALYPKII 240
QY 241 ODIEFTESNMRGGRHSIORIHCRSETSKGVYCLQYDDQKIVSGLDNTIKIMDKNTLCK 300
DB 241 ODIEFTESNMRGGRHSIORIHCRSETSKGVYCLQYDDQKIVSGLDNTIKIMDKNTLCK 300
QY 301 RILGHTGTSVLCLOQDERVIITGSSDSYVRVWDVNTGEMLNTLIHCEAVLHLRPNNGM 360
DB 301 RILGHTGTSVLCLOQDERVIITGSSDSYVRVWDVNTGEMLNTLIHCEAVLHLRPNNGM 360
QY 361 VTCSKDRSJAVWDMASPTDITLRVLYVGHRAAVNVVDPDKYIVASGDRITKWNSTJC 420
DB 361 VTCSKDRSJAVWDMASPTDITLRVLYVGHRAAVNVVDPDKYIVASGDRITKWNSTJC 420
QY 421 EFVRLTNGHKGRIACLOQRDRLVWSSGSDNTIRLWDIEGACLRVLEGBEELVRCIRPDN 480
DB 421 EFVRLTNGHKGRIACLOQRDRLVWSSGSDNTIRLWDIEGACLRVLEGBEELVRCIRPDN 480
QY 481 KRIVSGAYDGIKIKWDLVAALDPRAPAGTLCLRTLVHSGRVFRLOPDEFOQIVSSSHDT 540
DB 481 KRIVSGAYDGIKIKWDLVAALDPRAPAGTLCLRTLVHSGRVFRLOPDEFOQIVSSSHDT 540
QY 541 ILIWDPLNDPAAQAEPPSPSRITYISR 569
DB 541 ILIWDPLNDPAAQAEPPSPSRITYISR 569

RESULT 10
AAB48298
ID AAB48298 standard; protein; 569 AA.

XX AAB48298;

DT 02-APR-2001 (first entry)
DE Human ZF11 protein.

XX S-phase kinase associated protein; SKP1; SKP2; SKP2-like protein; ZF;
KW CUL-1; cullin; CDC53; p27; cyclin E; Max; Mad; c-Myc; MDM2; p53; Bax;
KW Bad; Bcl-2; tumour; cytosolic.

OS Homo sapiens.

PN WO200075184-A1.

PD 14-DEC-2000.

PF 05-JUN-2000; 2000WO-US015449.

PR 04-JUN-1999; 99US-0137494P.

PA (UYUA) UNIV YALE.

PI Zhang H, Tsvetkov LM, Kondo T;

XX WPI; 2001-061703/07.

DR N-PSDB; AAC84610.

PT Modulating polypeptide levels in a cell, diagnosing and treating tumor,
PT involves altering levels of proteins such as S-phase kinase associated
PT proteins 1, 2 and cullin/CDC53 proteins.

PS Claim 3; Page 130-132; 162pp; English.

CC The invention relates to methods of altering the polypeptide levels in a
CC cell, using proteins selected from S-phase kinase associated proteins 1
CC and 2 (SKP1, SKP2), SKP2-like proteins (ZF) and CUL-1 (a member of the
CC cullin/CDC53 family of proteins). The method is useful for altering the
CC level of p27, cyclin E, Max, Mad, c-Myc, MDM2, p53, Bax, Bad or Bcl-2
CC polypeptide in a cell. SKP2 and SKP2-like protein levels are useful for
CC detecting tumours, and in monitoring tumor treatment in a mammal. Agents
CC that modulate interactions between SKP and target proteins are useful for
CC treating tumours

CC Sequence 569 AA;

Query Match 99.8%; Score 3027; DB 4; Length 569;
Best Local Similarity 99.8%; Pred. No. 3.6e-285;
Matches 568; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDPAAVIOEALKKFNMSSEREDCNNGEPKRIPEKNSLRQTYNSCARCLCINOETVCLA 60
DB 1 MDPAAVIOEALKKFNMSSEREDCNNGEPKRIPEKNSLRQTYNSCARCLCINOETVCLA 60
QY 61 STAMKTENCVAKTKLANGTSSMIVPKORKLSASYEKEKELCVKYFEQMSBDOVEFEVHL 120
DB 61 STAMKTENCVAKTKLANGTSSMIVPKORKLSASYEKEKELCVKYFEQMSBDOVEFEVHL 120
QY 121 ISOMCHYOHGHINSYLYKPMLOQDFITLAPARGLDHIENILSYLDKSLCAAEIVCKEMY 180
DB 121 ISOMCHYOHGHINSYLYKPMLOQDFITLAPARGLDHIENILSYLDKSLCAAEIVCKEMY 180
QY 181 RYTSNGIMMKKLIEMVWRTDSIMRGLAERKGGYLLFKKPPDGNAPNSFYRALYPKII 240
DB 181 RYTSNGIMMKKLIEMVWRTDSIMRGLAERKGGYLLFKKPPDGNAPNSFYRALYPKII 240
QY 241 ODIEFTESNMRGGRHSIORIHCRSETSKGVYCLQYDDQKIVSGLDNTIKIMDKNTLCK 300
DB 241 ODIEFTESNMRGGRHSIORIHCRSETSKGVYCLQYDDQKIVSGLDNTIKIMDKNTLCK 300

QY 301 RILTGHTGSVLCQYDERVIITGSSDSTVRVMDVNTGEMLNTLIHCEAVLHLRFNNGM 360
DB 301 RILTGHTGSVLCQYDERVIITGSSDSTVRVMDVNTGEMLNTLIHCEAVLHLRFNNGM 360
QY 361 VTCSKDRSIAVWDMASPTDITLRLVVGRAAVNVDPDKXTIVASGDRITIKWNTSTC 420
DB 361 VTCSKDRSIAVWDMASPTDITLRLVVGRAAVNVDPDKXTIVASGDRITIKWNTSTC 420
QY 421 EFVRTLNGHKGIGACIQYRDLVVGSSDNTIRLMDIEGACLRVLEGHBEIVRCIRFDN 480
DB 421 EFVRTLNGHKGIGACIQYRDLVVGSSDNTIRLMDIEGACLRVLEGHBEIVRCIRFDN 480
QY 481 KRIVSGAYDGKIKWMDLVAAALDPRAPAGTLCRTLVHSGRVFRLOPDEFQIVSSSHDT 540
DB 481 KRIVSGAYDGKIKWMDLVAAALDPRAPAGTLCRTLVHSGRVFRLOPDEFQIVSSSHDT 540
QY 541 ILIWFPLNDPAAQAEPSPSPRTTYTISR 569
DB 541 ILIWFPLNDPAAQAEPSPSPRTTYTISR 569

RESULT 11
AAM00960
ID AAM00960 standard; protein; 608 AA.
XX
AC AAM00960;
XX
DT 01-OCT-2001 (first entry)
XX
DE Human bone marrow protein, SEQ ID NO: 436.
XX
KW Human; bone marrow; antiinflammatory; cyrostatic; neuroprotective;
KW antitviral; antibacterial; antifungal; anti-HIV; haemostatic;
KW immunosuppressive; gene therapy; cytokine cell proliferation;
KW cell differentiation modulator; immune disorder; infection; cancer;
KW human immunodeficiency virus; HIV; autoimmune disorder; haemophilia.
XX
OS Homo sapiens.
XX
PN WO200153453-A2.
XX
PD 26-JUL-2001.
XX
PF 23-DEC-2000; 2000WO-US034960.
XX
PR 23-DEC-1999; 99US-00471275.
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-00552317.
PR 20-JUN-2000; 2000US-00598042.
PR 19-JUL-2000; 2000US-00620312.
PR 03-AUG-2000; 2000US-00653450.
PR 14-SEP-2000; 2000US-00662191.
PR 19-OCT-2000; 2000US-00693036.
PR 30-NOV-2000; 2000US-0250583P.
XX
XX
PA (HYSE-) HYSEQ INC.
XX
PI Ford JE, Boyle BJ, Tang YT, Liu C, Aeundi V, Chen R, Ma Y,
PI Ren F, Wang J, Werhman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao Q;
PI Zhou P, Drmanac RT;
XX
DR WPI: 2001-488707/53.
XX
DR N-PSDB; AAH90079.
XX
PT Novel bone-marrow-expressed polynucleotides and polypeptides, useful for
PT treating e.g. cancer and immune deficiency disorders.
XX
PS Claim 10; Page 523-524; 648pp; English.
XX
CC The present sequence is one of 251 novel human polypeptides encoded by a
CC bone marrow-expressed polynucleotide. The polynucleotide and the
CC polypeptide encoded by it are useful in the treatment of various immune

CC deficiencies and disorders. The deficiencies and disorders may be
CC genetic, may be caused by a viral (e.g. HIV), bacterial or fungal
CC infection, or may result from an autoimmune disorder, a coagulation
CC disorder (e.g. haemophilia), inhibition of tumour cell proliferation,
CC suppression of an inflammatory response or treatment of a nervous system
CC disorder such as Alzheimer's disease. Detection of the presence or
CC increased expression of the polynucleotide or the protein it encodes is
CC useful for the diagnosis and/or prognosis of one or more types of cancer.
CC The polynucleotide and polypeptide can be used as nutritional sources or
CC supplements and in the screening of chemical compounds as potential drugs
XX
SQ Sequence 608 AA;
XX
Query Match 99.8%; Score 3027; DB 4; Length 608;
Best Local Similarity 99.6%; Pred No. 46-285;
Matches 567; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MDPAAVLOEKALEKFMNSEREDCNGEPKRIPEKNSLRQTVNSCARLCLNOETVCLA 60
DB 40 MDPAAVLOEKALEKFMNSEREDCNGEPKRIPEKNSLRQTVNSCARLCLNOETVCLA 99
QY 61 STAKTENCVAATKLANGTSSMIVPKOKLSASYEKEKELCVKYEPQWSESQVEFEHL 120
DB 100 STAKTENCVAATKLANGTSSMIVPKOKLSASYEKEKELCVKYEPQWSESQVEFEHL 159
QY 121 ISQCHYOHGHINSYLMKMLQDPFTALPARGLDHAENIISYLDKSLCAAEVCKEY 180
DB 160 ISQCHYOHGHINSYLMKMLQDPFTALPARGLDHAENIISYLDKSLCAAEVCKEY 219
QY 181 RYTSQGMMLKLEHVRVTDLSMRGLAERGGQYLFNKKPPDGNAPNSFYALYPKII 240
DB 220 RYTSQGMMLKLEHVRVTDLSMRGLAERGGQYLFNKKPPDGNAPNSFYALYPKII 279
QY 241 QDIETIESNMWGRHSLSORHCRSETSGVYCLQYDDQKIVSGLRDNTIKIKDKNTLBECK 300
DB 280 QDIETIESNMWGRHSLSORHCRSETSGVYCLQYDDQKIVSGLRDNTIKIKDKNTLBECK 339
QY 301 RILTGHTGSVLCQYDERVIITGSSDSTVRVMDVNTGEMLNTLIHCEAVLHLRFNNGM 360
DB 340 RILTGHTGSVLCQYDERVIITGSSDSTVRVMDVNTGEMLNTLIHCEAVLHLRFNNGM 399
QY 361 VTCSKDRSIAVWDMASPTDITLRLVVGRAAVNVDPDKXTIVASGDRITIKWNTSTC 420
DB 400 VTCSKDRSIAVWDMASPTDITLRLVVGRAAVNVDPDKXTIVASGDRITIKWNTSTC 459
QY 421 EFVRTLNGHKGIGACIQYRDLVVGSSDNTIRLMDIEGACLRVLEGHBEIVRCIRFDN 480
DB 460 EFVRTLNGHKGIGACIQYRDLVVGSSDNTIRLMDIEGACLRVLEGHBEIVRCIRFDN 519
QY 481 KRIVSGAYDGKIKWMDLVAAALDPRAPAGTLCRTLVHSGRVFRLOPDEFQIVSSSHDT 540
DB 520 KRIVSGAYDGKIKWMDLVAAALDPRAPAGTLCRTLVHSGRVFRLOPDEFQIVSSSHDT 579
QY 541 ILIWFPLNDPAAQAEPSPSPRTTYTISR 569
DB 580 ILIWFPLNDPAAQAEPSPSPRTTYTISR 608

RESULT 12
AAM78582
ID AAM78582 standard; protein; 605 AA.
XX
AC AAM78582;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human protein SEQ ID NO 1244.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.
XX

CC such as septic shock and bacterial infections; neurological diseases such
 CC as stroke-induced inflammation in neurons; neurodegenerative diseases and
 CC cancer. Accordingly, these complexes can be used for the development of
 CC pharmaceutical compositions that exhibit anti-inflammatory, antidiabetic,
 CC antineoplastic, cytostatic and antibacterial activities and can be used
 CC for gene therapy purposes. In particular, the invention further provides
 CC siRNA-oligonucleotides useful for inhibiting protein expression for in
 CC vitro or cell culture assays. This polypeptide is a human protein that
 CC can be used in combination with other proteins provided in the
 CC specification to form novel complexes of the TNF-alpha signalling pathway
 CC of the invention.

CC Sequence 605 AA;

Query Match 99.1%; Score 3006; DB 8; Length 605;
 Best Local Similarity 94.0%; Pred. No. 4,4e-283;
 Matches 569; Conservative 0; Mismatches 0; Indels 36; Gaps 1;

QY 1 MDPAAVAVLQEKALKFPM-----NSSRERDC 24
 DB 1 MDPAAVAVLQEKALKFPM-----NSSRERDC 60
 QY 25 NNGEPRKTIPEKNSLRQTYNSCARLCLNOETVCLASTAMKTENCVAKTKLANGTSSMTV 84
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 QY 85 PRQKLSASYEKEKELCVKTFEPMSSDOVEFEVHLISQMCHYOHGHSINSLKPMLOQRF 144
 DB 121 PRQKLSASYEKEKELCVKTFEPMSSDOVEFEVHLISQMCHYOHGHSINSLKPMLOQRF 180
 QY 145 ITALPARGDHIAENILSYLDAKSLCAAEVCEKEMRVTSDDGLMKELERVNRDTSLMR 204
 DB 181 ITALPARGDHIAENILSYLDAKSLCAAEVCEKEMRVTSDDGLMKELERVNRDTSLMR 240
 QY 205 GLAERRGMGOYLFPKKNPPDGNAPNSFYRALYPKIIQDIETTESNMRGSRHSIORIHCRS 264
 DB 241 GLAERRGMGOYLFPKKNPPDGNAPNSFYRALYPKIIQDIETTESNMRGSRHSIORIHCRS 300
 QY 265 EFSKGVYCLQYDDQKIVSGLRDNTIKIMDKNTLECKRIITGHTGSLVLCIQYDERVITTS 324
 DB 301 EFSKGVYCLQYDDQKIVSGLRDNTIKIMDKNTLECKRIITGHTGSLVLCIQYDERVITTS 360
 QY 325 SDSTVRVMDVTGEMLNTLIHCEAVLHLRFNNGMVTCSDKRSIAVMMASTDTITLRR 384
 DB 361 SDSTVRVMDVTGEMLNTLIHCEAVLHLRFNNGMVTCSDKRSIAVMMASTDTITLRR 420
 QY 385 VLVGHRRAAVNVDPDDKIYVSASGDRTIKVMNTSTCEFYRTLNGHKGRIACIQYDRRLV 444
 DB 421 VLVGHRRAAVNVDPDDKIYVSASGDRTIKVMNTSTCEFYRTLNGHKGRIACIQYDRRLV 480
 QY 445 SSSSDNTIRLMDIEGACLRVLEGEHELVRCTIRFDNKRIVSGAYDGKIKVMDLVAALDR 504
 DB 481 SSSSDNTIRLMDIEGACLRVLEGEHELVRCTIRFDNKRIVSGAYDGKIKVMDLVAALDR 540
 QY 505 APAGTLCIATLVESHSGRVFLQDFEQIVSSSHDDTILIMDFLNDPAAOAEPPRSPRTY 564
 DB 541 APAGTLCIATLVESHSGRVFLQDFEQIVSSSHDDTILIMDFLNDPAAOAEPPRSPRTY 600
 QY 565 TYISR 569
 DB 601 TYISR 605

RESULT 14

ID AAB12812 standard; protein; 569 AA.

XX AAB12812;

XX 27-NOV-2000 (first entry)

XX Mouse ubiquitin ligase FWD1 protein SEQ ID NO:2.

KW Ubiquitin ligase SCF complex; F-box protein; ubiquitination; Ikapab;
 KW beta-catenin; Skp1; Cull1; F-box motif; WD40 repeat motif; FWD1;
 KW gene therapy; colon cancer; beta-transducin repeat containing protein;
 KW beta-Trcp.

XX Mus musculus.

PN JP2000166542-A.

PD 20-JUN-2000.

PF 02-DEC-1998; 98JP-00343437.

PR 02-DEC-1998; 98JP-00343437.

PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

DR WPI; 2000-485550/43.

XX N-PSDB; AAA73131.

PT F-box protein of ubiquitin ligase SCF complex which promotes the
 PT ubiquitination of Ikapab or beta-catenin.

XX Claim 2; Page 9-10; 199p; Japanese.

CC The present invention describes an F-box motif protein of ubiquitin
 CC ligase SCF complex which promotes the ubiquitination of Ikapab or beta-
 CC catenin and is constituted by Skp1 protein, Cull1 protein and a complex
 CC (SCF complex) of F-box protein containing F-box motif and WD40 repeat
 CC motif and has the amino acid sequence of 45 residues (AAB12811) or one of
 CC two 569 residue sequences (AAB12812, which is mouse ubiquitin ligase FWD1
 CC protein) and (AAB12813, which is human beta-transducin repeat containing
 CC protein (beta-Trcp)). The F-box protein can be used for the gene therapy
 CC of colon cancer by being recombined to a virus vector

XX Sequence 569 AA;

Query Match 98.8%; Score 2997; DB 3; Length 569;
 Best Local Similarity 98.6%; Pred. No. 3e-282;
 Matches 561; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

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 DB 1 MDPAAVAVLQEKALKFPMSSEREDCNNGEPRKTIPEKNSLRQTYNSCARLCLNOETVCL 60
 QY 61 STAMKTENCVAKTKLANGTSSMTVPRKRLSASYEKEKELCVKTFEPMSSDOVEFEVHL 120
 DB 61 STAMKTENCVAKTKLANGTSSMTVPRKRLSASYEKEKELCVKTFEPMSSDOVEFEVHL 120
 QY 121 ISQMCHYOHGHSINSLKPMLOQRFITLAPGLDHIENILSYLDAKSLCAAEVCEKEM 180
 DB 121 ISQMCHYOHGHSINSLKPMLOQRFITLAPGLDHIENILSYLDAKSLCAAEVCEKEM 180
 QY 181 RVTSDGMLMKELIEMVTRTSLMRGLAERRGMGOYLFPKKNPPDGNAPNSFYRALYPKII 240
 DB 181 RVTSDGMLMKELIEMVTRTSLMRGLAERRGMGOYLFPKKNPPDGNAPNSFYRALYPKII 240
 QY 241 QDIETTESNMRGSRHSIORIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIMDKNTLECK 300
 DB 241 QDIETTESNMRGSRHSIORIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIMDKNTLECK 300
 QY 301 RILTGHTGSLVLCIQYDERVITTSDDSTVRVMDVTGEMLNTLIHCEAVLHLRFNNGM 360
 DB 301 RILTGHTGSLVLCIQYDERVITTSDDSTVRVMDVTGEMLNTLIHCEAVLHLRFNNGM 360
 QY 361 VTCSKDRSIAVWMASTDTITLRLVVGHRRAAVNVDPDDKIYVSASGDRTIKVMNTSTC 420
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 QY 421 EFVRTLNGHKGRIACIQYDRRLVVGSSDNTIRLMDIEGACLRVLEGEHELVRCTIRFDN 480
 DB 421 EFVRTLNGHKGRIACIQYDRRLVVGSSDNTIRLMDIEGACLRVLEGEHELVRCTIRFDN 480

QY 481 KRIVGAYDGKIKVMDLVAALDPAPAGTLCRLTVHSGRVFLQDFEFOIVSSSHDT 540
 DB 481 KRIVGAYDGKIKVMDLVAALDPAPAGTLCRLTVHSGRVFLQDFEFOIVSSSHDT 540
 QY 541 ILIWDFLNDPAAQAEPSPSPSRRTYTYISR 569
 DB 541 ILIWDFLNDPAAQAEPSPSPSRRTYTYISR 569

RESULT 15

AA83254
 ID AAY83254 standard; protein; 569 AA.

AC AAY83254;

DT 16-AUG-2000 (first entry)

DE F-box protein FWD1p.

KW Ubiquitin ligase; SCF; F-box protein; targeted degradation;

KW destabilization; proteolysis; drug discovery; gene therapy; cancer;

KW oncoprotein; Huntington's disease; gene knockout; delivery systems;

KW mouse; ss.

OS Mus musculus.

PN WO200022110-A2.

PD 20-APR-2000.

PF 08-OCT-1999; 99WO-US023705.

PR 09-OCT-1998; 98US-0103787P.

PA (HARD) HARVARD COLLEGE.

PI Zhou P, Howley P;

DR WPI, 2000-317970/27.

DR N-PSDB; AA293714.

PT Targeting degradation of polypeptide useful for treating cancer and other

PT proliferative disorders, involves conjugating polypeptide with ubiquitin

PT protein ligase or inhibiting ubiquitination using organic compound.

PS Claim 9; Page 184-185; 185pp; English.

XX The F-box proteins are a family of ubiquitin ligases (SCF ubiquitin

XX ligases) which can be used for the targeted degradation of a target

XX polypeptide in vivo. Targeted degradation is achieved by expressing the

XX ubiquitin ligase in a cell linked to the interaction domain of the target

XX polypeptide and thereby recruiting the target polypeptide to the

XX the level of a target polypeptide and for creating and expressing a

XX destabilized polypeptide which is subjected to SCF mediated proteolysis.

XX degrading any desired protein in a cell is useful for preventing or

XX treating diseases caused by the presence of abnormal amount of the

XX specific polypeptides, for drug discovery and for gene therapy. Diseases

XX treated include cancer, by degradation of oncoproteins, Huntington's

XX disease, other proliferative disorders and microbial infections. The

XX method provides a quick and easy alternative to gene knockout technology.

XX The target polypeptide can be degraded at all stages, or a specific

XX stage, of development in the mature animal

SQ Sequence 569 AA;

Query Match 98.8%; Score 2997; DB 3; Length 569;

Best Local Similarity 98.6%; Pred No. 3e-282; Mismatches 5; Indels 0; Gaps 0;

Matches 561; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 MDPAAVAVIQEALKKFMNSSEKDCNNGEPKRIPEKNSLRQTYNSCARLCTINQETVCLTA 60

DB 1 MDPAAVAVIQEALKKFMNSSEKDCNNGEPKRIPEKNSLRQTYNSCARLCTINQETVCLT 60

QY 61 STAKTENCVAKTKLANGTSSMTIVPKORKLSASYEKKEKLCVKKFEQMSSEDOVEFEHL 120
 DB 61 STAKTENCVAKTKLANGTSSMTIVPKORKLSASTEKEKLCVKFEQMSSEDOVEFEHL 120
 QY 121 ISQCHYQHGHINSYLKPMQLQDFITLPAAGLDHIAENILSYLDAKSLCAELVCCKEY 180
 DB 121 ISQCHYQHGHINSYLKPMQLQDFITLPAAGLDHIAENILSYLDAKSLCAELVCCKEY 180
 QY 181 RVTSDGMLMKKLIERRMVRTSLMRGLAERGGQYLFKNRPDGNAPNSFYRLAYKII 240
 DB 181 RVTSDGMLMKKLIERRMVRTSLMRGLAERGGQYLFKNRPDGNAPNSFYRLAYKII 240
 QY 241 QDIETISNMRCGRHSLORHCRSETSKGYVCLQYDDQKIVSGLRDNTIKIMDNTIECK 300
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 DB 241 QDIETISNMRCGRHSLORHCRSETSKGYVCLQYDDQKIVSGLRDNTIKIMDNTIECK 300
 QY 301 RILGHTGSVLCQYDERVIIITSSDSTVRVMDVNTGEMINTLIHCEAVLHLRFNNGM 360
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 QY 361 VTGSKDRIAWMDASPTDITLRAVYVGHRAAVNVDPDDKTIYASAGDRTIKWNTSTC 420
 DB 361 VTGSKDRIAWMDASPTDITLRAVYVGHRAAVNVDPDDKTIYASAGDRTIKWNTSTC 420
 QY 421 EFVRTLNGHKGRIACLOYRDLVYVSSSDNTIRLMDIECGACULVLRGHEELVRCIFPDN 480
 DB 421 EFVRTLNGHKGRIACLOYRDLVYVSSSDNTIRLMDIECGACULVLRGHEELVRCIFPDN 480
 QY 481 KRIVGAYDGKIKVMDLVAALDPAPAGTLCRLTVHSGRVFLQDFEFOIVSSSHDT 540
 DB 481 KRIVGAYDGKIKVMDLVAALDPAPAGTLCRLTVHSGRVFLQDFEFOIVSSSHDT 540
 QY 541 ILIWDFLNDPAAQAEPSPSPSRRTYTYISR 569
 DB 541 ILIWDFLNDPAAQAEPSPSPSRRTYTYISR 569

Search completed: April 25, 2005, 16:34:17
 Job time : 174 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 25, 2005, 16:06:41 / Search time 25 Seconds
(without alignments)
1699.013 Million cell updates/sec

Title: US-09-415-795-4

Perfect score: 3034

Sequence: 1 MDPAAVAVQEKALFKMNSSE.....PAAQAEPPPSRTYTYISR 569

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
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6: /cgn2_6/ptodata/1/1aa/6D_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3034	100.0	569	4	US-09-832-161-18 Sequence 18, Appl
2	3034	100.0	569	4	US-09-385-219A-2 Sequence 2, Appl
3	3034	100.0	569	4	US-09-601-168B-2 Sequence 2, Appl
4	2582.5	85.1	517	1	US-08-190-802A-30 Sequence 30, Appl
5	2582.5	85.1	517	3	US-08-477-346-30 Sequence 30, Appl
6	2582.5	85.1	517	3	US-08-473-089-30 Sequence 30, Appl
7	2582.5	85.1	517	3	US-08-487-072A-30 Sequence 30, Appl
8	2384.5	78.6	542	4	US-09-832-161-16 Sequence 16, Appl
9	644.5	21.2	626	4	US-09-213-888-21 Sequence 21, Appl
10	644.5	21.2	626	4	US-09-328-877D-21 Sequence 21, Appl
11	640	21.1	540	4	US-09-213-888-7 Sequence 7, Appl
12	640	21.1	540	4	US-09-213-888-10 Sequence 10, Appl
13	640	21.1	540	4	US-09-328-877D-7 Sequence 7, Appl
14	640	21.1	540	4	US-09-328-877D-10 Sequence 10, Appl
15	640	21.1	540	4	US-09-213-888-6 Sequence 6, Appl
16	640	21.1	545	4	US-09-328-877D-6 Sequence 6, Appl
17	640	21.1	553	4	US-09-213-888-5 Sequence 5, Appl
18	640	21.1	553	4	US-09-328-877D-5 Sequence 5, Appl
19	640	21.1	559	4	US-09-213-888-9 Sequence 9, Appl
20	640	21.1	559	4	US-09-328-877D-9 Sequence 9, Appl
21	640	21.1	589	4	US-09-213-888-8 Sequence 8, Appl
22	640	21.1	589	4	US-09-328-877D-8 Sequence 8, Appl
23	640	21.1	592	4	US-09-213-888-4 Sequence 4, Appl
24	640	21.1	592	4	US-09-328-877D-4 Sequence 4, Appl
25	640	21.1	627	4	US-09-213-888-3 Sequence 3, Appl
26	640	21.1	627	4	US-09-328-877D-3 Sequence 3, Appl
27	640	21.1	666	4	US-09-213-888-27 Sequence 27, Appl

28	640	21.1	666	4	US-09-328-877D-27	Sequence 27, Appl
29	640	21.1	669	4	US-09-213-888-25	Sequence 25, Appl
30	640	21.1	669	4	US-09-328-877D-25	Sequence 25, Appl
31	545	18.0	640	4	US-09-177-165A-30	Sequence 30, Appl
32	520	17.1	587	3	US-08-899-578-2	Sequence 2, Appl
33	419.5	13.8	376	4	US-09-248-796A-14173	Sequence 14173, A
34	399	13.2	779	1	US-08-190-802A-32	Sequence 32, Appl
35	399	13.2	779	3	US-08-477-346-32	Sequence 32, Appl
36	399	13.2	779	3	US-08-473-089-32	Sequence 32, Appl
37	399	13.2	779	4	US-08-487-072A-32	Sequence 32, Appl
38	399	13.2	779	4	US-09-177-165A-29	Sequence 29, Appl
39	399	13.2	779	4	US-09-538-092-264	Sequence 264, App
40	392	12.9	732	3	US-08-914-999-8	Sequence 8, Appl
41	359.5	11.8	373	4	US-09-248-796A-18953	Sequence 18953, A
42	354	11.7	409	2	US-08-283-917-3	Sequence 3, Appl
43	354	11.7	409	2	US-08-961-716-3	Sequence 3, Appl
44	354	11.7	409	4	US-09-538-092-1119	Sequence 1119, Ap
45	354	11.7	410	2	US-08-283-917-9	Sequence 9, Appl

ALIGNMENTS

RESULT 1									
US-09-832-161-18									
Sequence 18, Application US/09832161									
Patent No. 6656713									
GENERAL INFORMATION:									
APPLICANT: Manning, Anthony M.									
APPLICANT: Mercurio, Frank									
APPLICANT: Amle, Sharon									
APPLICANT: Ben-Neriah, Yinnon									
APPLICANT: Davis, Matti									
APPLICANT: Hatzuba, Ada									
APPLICANT: Lavon, Iris									
APPLICANT: Yaron, Avraham									
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING ACTIVATION OF									
FILE REFERENCE: 860098.427									
CURRENT FILING DATE: 2001-04-09									
PRIOR APPLICATION NUMBER: 09/210,060									
PRIOR FILING DATE: 1998-12-10									
NUMBER OF SEQ ID NOS: 30									
SOFTWARE: PatentIn Ver. 2.0									
SEQ ID NO 18									
LENGTH: 569									
TYPE: PRT									
ORGANISM: Homo sapiens									
US-09-832-161-18									
Query Match									
Best Local Similarity 100.0%; Score 3034; DB 4; Length 569;									
Matches 569; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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DB	1	MDPAAVAVQEKALFKMNSSE	RED	CN	GGPRKII	PEKSLA	Q	T	NSCARL
QY	61	STAKTEVCVAKTKLAN	GS	SMI	VPKOK	KL	S	AS	YEKEKEL
DB	61	STAKTEVCVAKTKLAN	GS	SMI	VPKOK	KL	S	AS	YEKEKEL
QY	121	ISOMCHYGHGINSY	LK	PM	ORD	FT	AL	P	ARGL
DB	121	ISOMCHYGHGINSY	LK	PM	ORD	FT	AL	P	ARGL
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DB	181	RVTS	GM	KL	IR	MT	DS	L	MR
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DB	241	ODIET	BS	N	MR	CG	HS	L	OR

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RESULT 2
US-09-385-219A-2
; Sequence 2, Application US/09385219A
; Patent No. 6720181
; GENERAL INFORMATION:
; APPLICANT: Chiant, D.
; APPLICANT: Pagano, M.
; APPLICANT: Latres, E.
; TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS
; FILE REFERENCE: 5914-081
; CURRENT APPLICATION NUMBER: US/09/385,219A
; CURRENT FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/098,355
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 60/118,568
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: 60/124,449
; PRIOR FILING DATE: 1999-03-15
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-385-219A-2

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Query Match      100.0%; Score 3034; DB 4; Length 569;
Best Local Similarity 100.0%; Pred. No. 5,8e-314;
Matches 569; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      241  ODIEETESNWRGSRSLQRIHCRSETSKGVYCLQYDDQKIVSGLADNTIKIMDKNTLECK 300
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RESULT 3
US-09-601-168B-2
; Sequence 2, Application US/09601168B
; Patent No. 6730486
; GENERAL INFORMATION:
; APPLICANT: BENAROUS, Richard
; APPLICANT: MARGOTTIN, Florence
; APPLICANT: DURAND, Hervé
; APPLICANT: ARENZANA SEISDEDOS, Fernando
; APPLICANT: KROLL, Mathias
; APPLICANT: CONDORCET, Jean-Paul
; TITLE OF INVENTION: Human beta-Ttcp protein
; FILE REFERENCE: 935.38812X00
; CURRENT APPLICATION NUMBER: US/09/601,168B
; CURRENT FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: PCT/FR99/00196
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: FR98 01100
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: FR98 15545
; PRIOR FILING DATE: 1998-12-09
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent In Ver. 2.1 and manually
; SEQ ID NO 2
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence : cDNA
US-09-601-168B-2

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Query Match      100.0%; Score 3034; DB 4; Length 569;
Best Local Similarity 100.0%; Pred. No. 5,8e-314;
Matches 569; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  MDPAAVLQEKALKFMNSEREDCNGEPKRIPEKNSLRQTYNSCARLCLNGETVCLA 60
      |||
Db      1  MDPAAVLQEKALKFMNSEREDCNGEPKRIPEKNSLRQTYNSCARLCLNGETVCLA 60
      |||
Qy      61  STAKTENCVAKTLANGTSSMIVPKORKLSASYEKEKELCVKFEQWSESQVEFVEHL 120
      |||
Db      61  STAKTENCVAKTLANGTSSMIVPKORKLSASYEKEKELCVKFEQWSESQVEFVEHL 120
      |||
Qy      121  ISOMCHYOHGHINSYLKPMLOQDFITLAPARGLDHAENILSYLDKASLCAAEIVCKEMY 180
      |||
Db      121  ISOMCHYOHGHINSYLKPMLOQDFITLAPARGLDHAENILSYLDKASLCAAEIVCKEMY 180
      |||
Qy      181  RVTSDGMLMKULIERMVRTDSLWRGLAERBGQYLFKNKPPDGNAPPNSFYRALYPKII 240
      |||
Db      181  RVTSDGMLMKULIERMVRTDSLWRGLAERBGQYLFKNKPPDGNAPPNSFYRALYPKII 240
      |||

```

QY 241 ODIEETIESNMRCGRHSLOIRHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIMDKNTLECK 300
 DB 241 ODIEETIESNMRCGRHSLOIRHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIMDKNTLECK 300
 QY 301 RLITHTGTSVLCLOYDERVITIGSSDSIVRVNDVTGEMLNTLIHCEAVLHFRNNGMM 360
 DB 301 RLITHTGTSVLCLOYDERVITIGSSDSIVRVNDVTGEMLNTLIHCEAVLHFRNNGMM 360
 QY 361 VTCSKORSIAVWDMSPDITILRVLVGHRVAVNVDPDDKIVASGDRITIKWNTSTC 420
 DB 361 VTCSKORSIAVWDMSPDITILRVLVGHRVAVNVDPDDKIVASGDRITIKWNTSTC 420
 QY 421 BEVRLTNGHKRGIAICLOYRDLRVSGSSDNTIRLMDIEGACLRVLEGHBEIVRCIRPDN 480
 DB 421 BEVRLTNGHKRGIAICLOYRDLRVSGSSDNTIRLMDIEGACLRVLEGHBEIVRCIRPDN 480
 QY 481 KRIVGAYDGKIRKVDLVAALDPRAAGTLCRTLVHSGRVFRLQDFEQIVSSSHDT 540
 DB 481 KRIVGAYDGKIRKVDLVAALDPRAAGTLCRTLVHSGRVFRLQDFEQIVSSSHDT 540
 QY 541 ILIMFLNDPRAOAPRPSRSTTYTISR 569
 DB 541 ILIMFLNDPRAOAPRPSRSTTYTISR 569

RESULT 4 US-08-190-802A-30

; Sequence 30, Application US/08190802A
 ; Patent No. 5519003
 ; GENERAL INFORMATION:
 ; APPLICANT: Mochly-Rosen, Daria
 ; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
 ; NUMBER OF SEQUENCES: 265
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dehlinger & Associates
 ; STREET: P. O. Box 60850
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94306-0850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: IBM PC compatible
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/190,802A
 ; FILING DATE: 01-FEB-1994
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fabian, Gary R.
 ; REGISTRATION NUMBER: 33,875
 ; REFERENCE/DOCKET NUMBER: 8600-0139
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 324-0860
 ; TELEFAX: (415) 324-0960
 ; INFORMATION FOR SEQ ID NO: 30:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 517 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: peptide
 ; HYPOTHEICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; INDIVIDUAL ISOLATE: BETA TRCP, Fig. 13
 ; US-08-190-802A-30

Query Match 85.1%; Score 2582.5; DB 1; Length 517;
 Best Local Similarity 91.4%; Pred. No. 6.5e-266;
 Matches 487; Conservative 7; Mismatches 8; Indels 31; Gaps 2;

QY 18 S SEREDCNNGEPPRKIIPEKNSLRQTVNSCARLCLNGETVCLASTAMKTENCVAKTKLAN 77
 DB 13 ASEREDCNNGEPPRKIIPEKNSLRQTVNSCARLCLNGETVCLASTAMKTENCVAKTKLAN 77
 QY 78 GTSSMIVKORKLSASYEKELCVKYPEQWSESDQVEVHLISQMHYGHGINSYLK 137
 DB 43 GTSSMIVKORKLSANYEKEKELCVKYPEQWSESDQVEVHLISQMHYGHGINTYLK 102
 QY 138 PMLQDPFTTALPARGLDIAENIISYLDKSLCAAEVCKEWMYRTSGMLMKKILERNV 197
 DB 103 PMLQDPFTTALPARGLDIAENIISYLDKSLCAAEVCKEWMYRTSGMLMKKILERNV 162
 QY 198 RTDSLNRGLAARBGQVLFNKKPPDGNAPNSFPAIYPRKIIDIEETIESNMRCGRHSI 257
 DB 163 RTDSLNRGLAARBGQVLFNKKPPDGNAPNSFPAIYPRKIIDIEETIESNMRCGRHSI 222
 QY 258 QRHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIMDKNTLECKRLTNGHTGTSVLCLOYDE 317
 DB 223 QRHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIMDKNTLECKRLTNGHTGTSVLCLOYDE 282
 QY 318 RVITIGSSDSIVRVNDVTGEMLNTLIHCEAVLHFRNNGMMVTCSDORSIAVWDMASP 377
 DB 283 RVITIG-SDSTVRVNDVTGEMLNTLIHCEAVLHFRNNGMMVTCSDORSIAVWDMASA 341
 QY 378 TDITLRRVLVGHRVAVNVDPDDKIVASGDRITIKWNTSTCEVRLTNGHKRGIAICLO 437
 DB 342 TDITLRRVLVGHRVAVNVDPDDKIVASGDRITIKWNTSTCEVRLTNGHKRGIAICLO 401
 QY 438 YRDLRVSGSSDNTIRLMDIEGACLRVLEGHBEIVRCIRPDNKRIVSGAYDGKIKVDL 497
 DB 402 YRDLRVSGSSDNTIRLMDIEGACLRVLEGHBEIVRCIRPDNKRIVSGAYDGKIKVDL 461
 QY 498 VVALDPRAAGTLCRTLVHSGRVFRLQDFEQIVSSSHDTIILIMFLNDP 550
 DB 462 VVALDPRAAGTLCRTLVHSGRVFRLQDFEQIVSSSHDTIILIMFLNDP 514

RESULT 5

US-08-477-346-30
 ; Sequence 30, Application US/08477346
 ; Patent No. 6262023
 ; GENERAL INFORMATION:
 ; APPLICANT: Mochly-Rosen, Daria
 ; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
 ; NUMBER OF SEQUENCES: 265
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Morrison & Foerster
 ; STREET: 2000 Pennsylvania Avenue, NW
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20006-1812
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: IBM PC compatible
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/477,346
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/487,072
 ; FILING DATE: 07-JUN-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: MURASHIGE, KATE H.
 ; REGISTRATION NUMBER: 29,959
 ; REFERENCE/DOCKET NUMBER: 2550-0025.20
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 887-1500


```
TELEFAX: (202) 887-0763
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 517 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: BETA TRCP, Fig. 13
US-08-477-346-30

Query Match      85.1%; Score 2582.5; DB 3; Length 517;
Best Local Similarity 91.4%; Pred. No. 6.5e-266;
Matches 487; Conservative 7; Mismatches 8; Indels 31; Gaps 2;

QY 18 SSEREDCNGEPKRIPEKNSLRQYNSCARLCLNOETVCLASTAMKTENCVAKTCLAN 77
DB 13 ASEREDCNRDEPPKRIITEKNTRLRQ-----TKLAN 42
QY 78 GTSSMIVKQKRLSAYEKEKELCVKYPEOWSESDQVEFVEHLISOMCHYOHGHINSYLK 137
DB 43 GTSSMIVKQKRLSAYEKEKELCVKYPEOWSESDQVEFVEHLISRMCHYOHGHINTYLYK 102
QY 138 PMLORDFITLAPARGLDHIAENILSYLDAKSLCAAEIVCKEWMYRVTSQMLMKKLIERMV 197
DB 103 PMLORDFITLAPARGLDHIAENILSYLDAKSLCAAEIVCKEWMYRVTSQMLMKKLIERMV 162
QY 198 RTDSLWRLGLAERRMGQYLFKNKPPDGNAPNSFYRALYPKLIODIETIESNMRGGRHSL 257
DB 163 RTDSLWRLGLAERRMGQYLFKNKPPDGNAPNSFYRALYPKLIODIETIESNMRGGRHSL 222
QY 258 QRHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIMDKNTLECKRILTGHTGSVYCLQYDE 317
DB 223 QRHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIMDKNTLECKRILTGHTGSVYCLQYDE 282
QY 318 RVIIITGSSDSTVRWVDNTGEMLNTLIHCEAVLHLRFNNGMMVTCSDKRSIAVDMAS 377
DB 283 RVIIITG-SDSTVRWVDNTGEMLNTLIHCEAVLHLRFNNGMMVTCSDKRSIAVDMASA 341
QY 378 TDITLRRVIVGHRAAVNVVDPDDKYIVSASGDRITIKWNTSTCEFYVTLNGHKGRIACIQ 437
DB 342 TDITLRRVIVGHRAAVNVVDPDDKYIVSASGDRITIKWNTSTCEFYVTLNGHKGRIACIQ 401
QY 438 YRDLRVVSGSSDNTIRLMDIEGACLRVLEGHIEELVRCIRPDNKRIVSAGVDGKIKWDL 497
DB 402 YRDLRVVSGSSDNTIRLMDIEGACLRVLEGHIEELVRCIRPDNKRIVSAGVDGKIKWDL 461
QY 498 VAALDPRAPAGTLCRLTVHSGRVFRLQDFEFOIVSSSHDDTILIMDFLNDP 550
DB 462 VAALDPRAPAGTLCRLTVHSGRVFRLQDFEFOIVSSSHDDTILIMDFLNDP 514

RESULT 6
US-08-473-089-30
; Sequence 30, Application US/08473089
; Patent No. 6342368
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
```

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COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/473,089
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2550-0025.22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 517 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: BETA TRCP, Fig. 13
US-08-473-089-30

Query Match      85.1%; Score 2582.5; DB 3; Length 517;
Best Local Similarity 91.4%; Pred. No. 6.5e-266;
Matches 487; Conservative 7; Mismatches 8; Indels 31; Gaps 2;

QY 18 SSEREDCNGEPKRIPEKNSLRQYNSCARLCLNOETVCLASTAMKTENCVAKTCLAN 77
DB 13 ASEREDCNRDEPPKRIITEKNTRLRQ-----TKLAN 42
QY 78 GTSSMIVKQKRLSAYEKEKELCVKYPEOWSESDQVEFVEHLISOMCHYOHGHINSYLK 137
DB 43 GTSSMIVKQKRLSAYEKEKELCVKYPEOWSESDQVEFVEHLISRMCHYOHGHINTYLYK 102
QY 138 PMLORDFITLAPARGLDHIAENILSYLDAKSLCAAEIVCKEWMYRVTSQMLMKKLIERMV 197
DB 103 PMLORDFITLAPARGLDHIAENILSYLDAKSLCAAEIVCKEWMYRVTSQMLMKKLIERMV 162
QY 198 RTDSLWRLGLAERRMGQYLFKNKPPDGNAPNSFYRALYPKLIODIETIESNMRGGRHSL 257
DB 163 RTDSLWRLGLAERRMGQYLFKNKPPDGNAPNSFYRALYPKLIODIETIESNMRGGRHSL 222
QY 258 QRHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIMDKNTLECKRILTGHTGSVYCLQYDE 317
DB 223 QRHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIMDKNTLECKRILTGHTGSVYCLQYDE 282
QY 318 RVIIITGSSDSTVRWVDNTGEMLNTLIHCEAVLHLRFNNGMMVTCSDKRSIAVDMAS 377
DB 283 RVIIITG-SDSTVRWVDNTGEMLNTLIHCEAVLHLRFNNGMMVTCSDKRSIAVDMASA 341
QY 378 TDITLRRVIVGHRAAVNVVDPDDKYIVSASGDRITIKWNTSTCEFYVTLNGHKGRIACIQ 437
DB 342 TDITLRRVIVGHRAAVNVVDPDDKYIVSASGDRITIKWNTSTCEFYVTLNGHKGRIACIQ 401
QY 438 YRDLRVVSGSSDNTIRLMDIEGACLRVLEGHIEELVRCIRPDNKRIVSAGVDGKIKWDL 497
DB 402 YRDLRVVSGSSDNTIRLMDIEGACLRVLEGHIEELVRCIRPDNKRIVSAGVDGKIKWDL 461
QY 498 VAALDPRAPAGTLCRLTVHSGRVFRLQDFEFOIVSSSHDDTILIMDFLNDP 550
DB 462 VAALDPRAPAGTLCRLTVHSGRVFRLQDFEFOIVSSSHDDTILIMDFLNDP 514

RESULT 7
US-08-487-072A-30
; Sequence 30, Application US/08487072A
; Patent No. 6423684
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
```

APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,072A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 517 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP, Fig. 13
US-08-487-072A-30

Query Match 85.1%; Score 2582.5; DB 4; Length 517;
Best Local Similarity 91.4%; Pred. No. 6.5e-266;
Matches 487; Conservative 7; Mismatches 8; Indels 31; Gaps 2;
QY 18 S E R D C N N G E P P R K I I P E K N S L R Q T Y N S C A R L C I N Q E T V C L A S T A M K T E N C V A T K L A N 77
DB 13 A S E R D C N N G E P P R K I I T E K N T L R Q-----T K L A N 42
QY 78 G T S S M I V P K O R K L S A S Y E K E K E L C V Y F P O M S E S D Q V E F E H L I S O M C H Y O H G I N S Y L K 137
DB 43 G T S S M I V P K O R K L S A N Y E K E K E L C V Y F P O M S E C Q V E F E H L I S R M C H Y O H G I N T Y L K 102
QY 138 P M L Q R D F T A L P A R G L D H I A E N I L S Y L D A K S I C A A L V C K E M Y R V T S D G M L M K K L I E R N V 197
DB 103 P M L Q R D F T A L P A R G L D H I A E N I L S Y L D A K S I C A A L V C K E M Y R V T S D G M L M K K L I E R N V 162
QY 198 R D S I M R G I A E R R G G O Y L F K N K P P D G N A P M S F Y R A L Y P K I I O D I E T I E S W M R G R S L 257
DB 163 R D S I M R G I A E R R G G O Y L F K N K P P D G K T P N S F Y R A L Y P K I I O D I E T I E S W M R G R S L 222
QY 258 Q R I H R S E T S K G V Y C L Q Y D D Q K I V S G L R D N T I K I M D K N T L E C K R I L T G H T G S V L C L Q Y D E 317
DB 223 Q R I H R S E T S K G V Y C L Q Y D D Q K I V S G L R D N T I K I M D K N T L E C K R I L T G H T G S V L C L Q Y D E 282
QY 318 R V I T I G S S D S T Y R V M D V N T G E M L A N T L I H H C E A V L H L R F N N G M V T C S K D R S I A V W D M A S P 377
DB 283 R V I T I G - S D S T Y R V M D V N T G E M L A N T L I H H C E A V L H L R F N N G M V T C S K D R S I A V W D M A S A 341
QY 378 T D I T L R V L V G H R A A V N V V D P D K I V S A S G R T I K W M N T S T C E V R T L N G H K R G I A C L Q 437
DB 342 T D I T L R V L V G H R A A V N V V D P D K I V S A S G R T I K W M N T S T C E V R T L N G H K R G I A C L Q 401
QY 438 Y R D L V S G S S D N T I R L M D I E G A C L R V L E G H E L V R C I R P D N K R I V S G A V D G K I K W M D L 497

DB 402 Y R D L V S G S S D N T I R L M D I E G A C L R V L E G H E L V R C I R P D N K R I V S G A V D G K I K W M D L 461
QY 498 V A A L D P R A P A G T L C L R T L V H S G R V R L Q F D E F Q V S S H D T I L I M P L A N P 550
DB 462 V A A L D P R A P A G T L C L R T L V H S G R V R L Q F D E F Q V S S H D T I L I M P L A N P 514
RESULT 8
US-09-832-161-16
Sequence 16, Application US/09832161
Patent No. 6656713
GENERAL INFORMATION:
APPLICANT: Manning, Anthony M.
APPLICANT: Mercurio, Frank
APPLICANT: Amit, Sharon
APPLICANT: Ben-Neriah, Yimon
APPLICANT: Davis, Matti
APPLICANT: Hatzubai, Ada
APPLICANT: Lavon, Iris
APPLICANT: Yaron, Avraham
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING ACTIVATION OF
TITLE OF INVENTION: NF-kB
FILE REFERENCE: 860098.427
CURRENT APPLICATION NUMBER: US/09/832,161
CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 09/210,060
PRIOR FILING DATE: 1998-12-10
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 16
LENGTH: 542
TYPE: PRT
ORGANISM: Homo sapiens
US-09-832-161-16
Query Match 78.6%; Score 2384.5; DB 4; Length 542;
Best Local Similarity 79.0%; Pred. No. 8.9e-245;
Matches 451; Conservative 48; Mismatches 41; Indels 31; Gaps 7;
QY 1 M D P A V L O E R A L K F M N S S E R D C N N G E P P R K I I P E K N S L R Q T Y N S C A R L C I N Q E T V C L A 60
DB 1 M E P - D S V I E D T I E I M C S-----V P-----S L M I G C A N L V-----S M C A L 36
QY 61 S--T M K T E N C V A T K L A N G T S S M I V P K O R K L S A S Y E K E K E L C V Y F P O M S E S D Q V E F E 118
DB 37 S C L O S M P S V R C L-----Q I S N G T S S V I V S R K R P S E G N Y O K E K O L C I Y F O M S E S D Q V E F E 93
QY 119 H L I S O M C H Y O H G I N S Y L K P M L Q R D F T A L P A R G L D H I A E N I L S Y L D A K S I C A A L V C K E 178
DB 94 H L I S M C H Y O H G I N S Y L K P M L Q R D F T A L P E Q G L D H I A E N I L S Y L D A R S I C A A L V C K E 153
QY 179 W Y R V T S D G M L M K K L I E R N V R T D S I M R G I A E R R G G O Y L F K N K P P D G N A P M S F Y R A L Y P K 238
DB 154 W O R V I S E G M L M K K L I E R N V R T D P L M K G L S E R G M D Q Y L F K R P T D G--P P N S F Y R S L Y P K 211
QY 229 I I O D I E T I E S W M R G R S L O R I H R S E T S K G V Y C L Q Y D D Q K I V S G L R D N T I K I M D K N T L E 298
DB 212 I I O D I E T I E S W M R G R H L O R I O C R S E N S K G V Y C L Q Y D D E K I I S G L R D N S I K I M D K T S L E 271
QY 299 C K R I L T G H T G S V L C L Q Y D E R V I T I G S S D S T Y R V M D V N T G E M L A N T L I H H C E A V L H L R F N N G 358
DB 272 C L K V I T I G H T G S V L C L Q Y D E R I V I T G S S S T Y R V M D V N T G E V A N T L I H H N E A V L H R F S N G 331
QY 359 M M V T C S K D R S I A V W D M A S P T D I T L R V L V G H R A A V N V V D P D K I V S A S G R T I K W M N T S 418
DB 332 L M V T C S K D R S I A V W D M A S A T D I T L R V L V G H R A A V N V V D P D K I V S A S G R T I K W M N T S 391
QY 419 T C E F V R T L N G H K R G I A C L Q Y D R L V S G S S D N T I R L M D I E G A C L R V L E G H E L V R C I R F 478
DB 392 T C E F V R T L N G H K R G I A C L Q Y D R L V S G S S D N T I R L M D I E G A C L R V L E G H E L V R C I R F 451
QY 479 D N K R I V S G A V D G K I K W M D L V A A L D P R A P A G T L C L R T L V H S G R V R L Q F D E F Q V S S H D 538

Db 452 DNKRIVSGAYDGIKIVMDLQALDPRAPASTLCLRTLVHSGRVRLQDFEQIISSHD 511
QY 539 DTLLIWDPLNDPAQAEPSPSRRTTYISR 569
Db 512 DTLLIWDPLNVPSPAQNETSPSRRTTYISR 542

RESULT 9
US-09-213-888-21
; Sequence 21, Application US/09213888A
; Patent No. 6638731
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Li, Jinhe
; APPLICANT: Pauley, Adele M.
; APPLICANT: Pharmacia & Upjohn Company
; TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
; FILE REFERENCE: 6142
; CURRENT APPLICATION NUMBER: US/09/213,888A
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 626
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 6 myc tagged
US-09-213-888-21

Query Match 21.2%; Score 644.5; DB 4; Length 626;
Best Local Similarity 30.1%; Pred. No. 3.1e-59;
Matches 169; Conservative 103; Mismatches 222; Indels 67; Gaps 15;

QY 8 LQEKALKFMSSEEDCNGEPPRKIIPEK--NSLRQ--TYNSCARLCLNOETVCLASTA 63
Db 53 MEQKLISEBDLNEMSLDGLTMEQKLISEBDLNEMSKRLDHGSEVRSPLGKPKCKVSEY 112
QY 64 MKNENCV-----AKTKLANGTSSMIVPKOKRLSASYEKEL--CVKYFEQWSSSD 112
Db 113 TSTTGLVPCSATPTTFEGDLRANQOG-----QQRRTTSVQPTGLQELKMFQSWSGPE 167
QY 113 QVEFEVHLISQWCHYQGHINSYLKPMLODFITLPAAGLDHIAENILSYLDAKSLCAA 172
Db 168 KTLALDELIDSCBPTQVHMMQVIEPQFRDFISLP---KELALVYLSFLEPKDLQQA 223
QY 173 ELVCKEYRVTSDDGMLMKKLIERNVRTDSLNRGLAE---RRGNGQYLFRNKRPPDGNAP 227
Db 224 AOTCRVYRILAEIDLMLREKCKE-----EGIDELPHIKRRK-----VIKGFTHSP 269
QY 228 PMSFYRALYPKIIODIETIESNMRGHRSLQRIHCRSETSKGVYCLQYDDQKIYSGLRDN 287
Db 270 WKSAY-----IRQ--HRIDTMRRGELKSPKV-LKGDHDHIVITCLOFGCNRIVSGSDN 320
QY 288 TIKIWDKNTLECKRIITLGHSTGSLCLQYDERVITIGSSSDTVRWVDVNTGEMLTLLIHC 347
Db 321 TLKWSAVTGKCLRTLVGHSTGWSQMRDNIISGSTDRTLKWNMAETGECIHITLYGHT 380
QY 348 EAVLHLRFNNGMVTCSKDRSLAVWDMASTPDIITLRVLYGHRVAANVVPDPPDKIYVSAS 407
Db 381 STVRCMHLHKKRVVSSGRATLRVMDIETGQCL---HVLMGHVAANVRCVQYDGRRVVSGA 437
QY 408 GDRITKWNVTSTCEFVTLNGHKRGIACTQYRDLVYSGSSDNTIRLMDIEGACLRVLE 467
Db 438 YDPMVKVMDPETETCITLQGHITNRVYSLQPDGIHVVSGLSDTISRWDVETGNCIHITLT 497
QY 468 GHEELVRCIRFDNRKRVISGAYDGKI KVMIDLVAALDPRAPAGTLCLRTLV---EHSGRVFR 524
Db 498 GHQSLTSGMELKDNILVSGNADSTYKIMDIKTG-----QCLQTLQGPBKQSAVTC 548
QY 525 LQDFEQIVSSSHDDTLLIWD 545

Db 549 LQFNKNFVITSSDDGTVKLMD 569

RESULT 10
US-09-328-877D-21
; Sequence 21, Application US/09328877D
; Patent No. 6730778
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Li, Jinhe
; APPLICANT: Pauley, Adele M.
; APPLICANT: Pharmacia & Upjohn Company
; TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
; FILE REFERENCE: 6142
; CURRENT APPLICATION NUMBER: US/09/328,877D
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 626
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 6 myc tagged
US-09-328-877D-21

Query Match 21.2%; Score 644.5; DB 4; Length 626;
Best Local Similarity 30.1%; Pred. No. 3.1e-59;
Matches 169; Conservative 103; Mismatches 222; Indels 67; Gaps 15;

QY 8 LQEKALKFMSSEEDCNGEPPRKIIPEK--NSLRQ--TYNSCARLCLNOETVCLASTA 63
Db 53 MEQKLISEBDLNEMSLDGLTMEQKLISEBDLNEMSKRLDHGSEVRSPLGKPKCKVSEY 112
QY 64 MKNENCV-----AKTKLANGTSSMIVPKOKRLSASYEKEL--CVKYFEQWSSSD 112
Db 113 TSTTGLVPCSATPTTFEGDLRANQOG-----QQRRTTSVQPTGLQELKMFQSWSGPE 167
QY 113 QVEFEVHLISQWCHYQGHINSYLKPMLODFITLPAAGLDHIAENILSYLDAKSLCAA 172
Db 168 KTLALDELIDSCBPTQVHMMQVIEPQFRDFISLP---KELALVYLSFLEPKDLQQA 223
QY 173 ELVCKEYRVTSDDGMLMKKLIERNVRTDSLNRGLAE---RRGNGQYLFRNKRPPDGNAP 227
Db 224 AOTCRVYRILAEIDLMLREKCKE-----EGIDELPHIKRRK-----VIKGFTHSP 269
QY 228 PMSFYRALYPKIIODIETIESNMRGHRSLQRIHCRSETSKGVYCLQYDDQKIYSGLRDN 287
Db 270 WKSAY-----IRQ--HRIDTMRRGELKSPKV-LKGDHDHIVITCLOFGCNRIVSGSDN 320
QY 288 TIKIWDKNTLECKRIITLGHSTGSLCLQYDERVITIGSSSDTVRWVDVNTGEMLTLLIHC 347
Db 321 TLKWSAVTGKCLRTLVGHSTGWSQMRDNIISGSTDRTLKWNMAETGECIHITLYGHT 380
QY 348 EAVLHLRFNNGMVTCSKDRSLAVWDMASTPDIITLRVLYGHRVAANVVPDPPDKIYVSAS 407
Db 381 STVRCMHLHKKRVVSSGRATLRVMDIETGQCL---HVLMGHVAANVRCVQYDGRRVVSGA 437
QY 408 GDRITKWNVTSTCEFVTLNGHKRGIACTQYRDLVYSGSSDNTIRLMDIEGACLRVLE 467
Db 438 YDPMVKVMDPETETCITLQGHITNRVYSLQPDGIHVVSGLSDTISRWDVETGNCIHITLT 497
QY 468 GHEELVRCIRFDNRKRVISGAYDGKI KVMIDLVAALDPRAPAGTLCLRTLV---EHSGRVFR 524
Db 498 GHQSLTSGMELKDNILVSGNADSTYKIMDIKTG-----QCLQTLQGPBKQSAVTC 548
QY 525 LQDFEQIVSSSHDDTLLIWD 545
Db 549 LQFNKNFVITSSDDGTVKLMD 569

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RESULT 11
US-09-213-888-7
; Sequence 7, Application US/09213888A
; Patent No. 6638731
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Li, Jinhe
; APPLICANT: Pauley, Adele M.
; APPLICANT: Pharmacia & Upjohn Company
; TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
; FILE REFERENCE: 6142
; CURRENT APPLICATION NUMBER: US/09/213,888A
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 7
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-213-888-7

Query Match      21.1%; Score 640; DB 4; Length 540;
Best Local Similarity 30.8%; Pred. No. 7,2e-59;
Matches 167; Conservative 92; Mismatches 211; Indels 72; Gaps 15;

QY      14 KFMNSEREDCNNGEPPKRIPEKNSLRQTYNSCARLCLNOBTVCIASTAMKTCNCAVKT 73
      4 KLDHSEVRSFSLGKKPKCV-----SEYTSSTGL-----VPCSA-----TPTTFGLD 45
DB      74 KLANGTSMIYKQKRLSAYEKEKEL--CYKFFQWSESDQVEVEHLISQMCHYQGH 131
      46 RAANGOG-----QQRRTTSVOPPTGLQEWLMFQSWGPEKLLADLIDSCPTQVGH 100
QY      132 INSYLKPMLODFITALPARGLDIAENILSYLDKSLCAAEIVCKEWRVYSDGMLWK 191
      101 MMQVIEPQDFQDFISLP---KELALYVLSFLEPKDLQAQTCRYRRIADMLMRE 156
DB      192 LIERNVRTDSLWRGLAE-----RQWGQYLFKNKPPDGNAPNSFYRALYPKIIODIETI 246
      157 KCKE-----EGIDELPHIKRRK-----VIKGFHSPWKSAY-----IRQ--HRI 194
QY      247 ESNWRCGRHSIORIHCRSETSKGVYCLQYDDOKIYSGLRDNTIKWDKNTLECKRIILGH 306
      195 DTNMRGELKSPKV-LKGHDHVITCLOFCGNRIYSGSDNTLKYWSAVTGKCLRTLVGH 253
DB      307 TGSVYLCQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHCEAVLHLRFNNGMVTYCSKD 366
      254 TGGWSSQMRDNIIISGSTDRTLKYMAETGECIHTLVGHTSTVRCMHLHERKRVSSGRD 313
QY      367 RSIAYWMAESPDTITLRLRVLVGHRAAVNVVDPDKYIVASAGDRTIKYWNSTCEFEVRL 426
      314 ATLRYWDIETGQCL---HVLGMHVAAYRCVQYDGRVYSGAYDFWVKWMDPETETCLHTL 370
DB      427 NGHRGIGACLOYRDLVYSGSSDNTIRLMDIECGACLRVLEGEHELVCIRPDNRIYSG 486
      371 QGHTNRVYSLQDFGIHVVGSLDTSIRWADVETGNCIHTLVGHOSLITSGMELKMDILVSG 430
QY      487 AYDGKIKYWDVAALDPAPAGTLCRLTV---EHSRGVRFLOPDEFOIVSSSHDITLI 543
      431 NADSTVKIWDITKG-----QCLQTLQGNPKHQSAVTCLOFNKXNVITISSDDGTIVKL 481
DB      544 WD 545
      482 WD 483

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; APPLICANT: Gurney, Mark E.
; APPLICANT: Li, Jinhe
; APPLICANT: Pauley, Adele M.
; APPLICANT: Pharmacia & Upjohn Company
; TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
; FILE REFERENCE: 6142
; CURRENT APPLICATION NUMBER: US/09/213,888A
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 10
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-213-888-10

Query Match      21.1%; Score 640; DB 4; Length 540;
Best Local Similarity 30.8%; Pred. No. 7,2e-59;
Matches 167; Conservative 92; Mismatches 211; Indels 72; Gaps 15;

QY      14 KFMNSEREDCNNGEPPKRIPEKNSLRQTYNSCARLCLNOBTVCIASTAMKTCNCAVKT 73
      4 KLDHSEVRSFSLGKKPKCV-----SEYTSSTGL-----VPCSA-----TPTTFGLD 45
DB      74 KLANGTSMIYKQKRLSAYEKEKEL--CYKFFQWSESDQVEVEHLISQMCHYQGH 131
      46 RAANGOG-----QQRRTTSVOPPTGLQEWLMFQSWGPEKLLADLIDSCPTQVGH 100
QY      132 INSYLKPMLODFITALPARGLDIAENILSYLDKSLCAAEIVCKEWRVYSDGMLWK 191
      101 MMQVIEPQDFQDFISLP---KELALYVLSFLEPKDLQAQTCRYRRIADMLMRE 156
DB      192 LIERNVRTDSLWRGLAE-----RQWGQYLFKNKPPDGNAPNSFYRALYPKIIODIETI 246
      157 KCKE-----EGIDELPHIKRRK-----VIKGFHSPWKSAY-----IRQ--HRI 194
QY      247 ESNWRCGRHSIORIHCRSETSKGVYCLQYDDOKIYSGLRDNTIKWDKNTLECKRIILGH 306
      195 DTNMRGELKSPKV-LKGHDHVITCLOFCGNRIYSGSDNTLKYWSAVTGKCLRTLVGH 253
DB      307 TGSVYLCQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHCEAVLHLRFNNGMVTYCSKD 366
      254 TGGWSSQMRDNIIISGSTDRTLKYMAETGECIHTLVGHTSTVRCMHLHERKRVSSGRD 313
QY      367 RSIAYWMAESPDTITLRLRVLVGHRAAVNVVDPDKYIVASAGDRTIKYWNSTCEFEVRL 426
      314 ATLRYWDIETGQCL---HVLGMHVAAYRCVQYDGRVYSGAYDFWVKWMDPETETCLHTL 370
DB      427 NGHRGIGACLOYRDLVYSGSSDNTIRLMDIECGACLRVLEGEHELVCIRPDNRIYSG 486
      371 QGHTNRVYSLQDFGIHVVGSLDTSIRWADVETGNCIHTLVGHOSLITSGMELKMDILVSG 430
QY      487 AYDGKIKYWDVAALDPAPAGTLCRLTV---EHSRGVRFLOPDEFOIVSSSHDITLI 543
      431 NADSTVKIWDITKG-----QCLQTLQGNPKHQSAVTCLOFNKXNVITISSDDGTIVKL 481
DB      544 WD 545
      482 WD 483

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RESULT 13
US-09-328-877D-7
; Sequence 7, Application US/09328877D
; Patent No. 6730778
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Li, Jinhe
; APPLICANT: Pauley, Adele M.
; APPLICANT: Pharmacia & Upjohn Company
; TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
; FILE REFERENCE: Encode Them

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; FILE REFERENCE: 6142
; CURRENT APPLICATION NUMBER: US/09/328,877D
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 7
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-328-877D-7

Query Match      21.1%; Score 640; DB 4; Length 540;
Best Local Similarity 30.8%; Pred. No. 7,2e-59;
Matches 167; Conservative 92; Mismatches 211; Indels 72; Gaps 15;

QY      14 KPNSSEREDCNNGEPKRIPEKNSLRQTNNSCARLCLNQETVCLASTAMKTENCVAKT 73
      4 KLDHSEVRSFSLGKKPCKV-----SEYTSITGL-----VPCSA-----TPTTFGDL 45
      74 KLANGSSMIVPKORKLSASVEKEKL--CVKYEQMSSESDQVEFVHLISQMGHYOHGH 131
      46 RAANGOG-----QQRRIITSVQPTGLOEMLMFQSWGPEKLLADBELIDSCPTQYKH 100
QY      132 INSYLKPMLOPDRFTALPARGLDHAENILSYLDAKSLCAAEIVCKEWYRVTSQDMLMKK 191
      101 MMQVIEPQFQDRDFISLSP---KELALVYLSFLEPKDLLQAQTCRYWRIIAEDNLLMRE 156
QY      192 LIEMVRTDSLWRGLAE---RRMGQOYLFKNKPPDGNAPNPSFYRALYFKTIQDIETI 246
      157 KCKE-----EGIDEPFLHKKRK-----VIRKGFHSPWKSAY-----IRQ--HRI 194
QY      247 ESNMRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIMDKNTLECKRIITGH 306
      195 DYNMRGELKSPKV-LKGHDHVITCLQPCGNRIYVSGSDNTILKWSAVTGKCLRTLVGH 253
QY      307 TGSVYLCLOYDERVIITGSSDSITRVWVDNTGEMLNTLIHCEAVLHLRFNNGMMVTCSKD 366
      254 TGVWSSQMRDNIILISGSTDRTLKVMNAETGECIHTLVGHTSTVACMHLHEKRVVSGRD 313
QY      367 RSIWVMDASPTDITTLRVLVGHRAAVNVDPDDKIVYSASGDTIKVMNTSTGEFRTL 426
      314 ATLRWDIETGQCL---HVLMGHVAARVCQYDGRVVSAGAYDFWVKWDPETETCLHTL 370
QY      427 NGHKRGIACTLOYRDLVWSSGSDNTIRLMDIEGACLRVLEGHELVLCIRFDNKRIVSG 486
      371 QGHTNRVYSLQPDGIHVVSGLDTSIRWVDVETGNCIHTLTHGSLTSGMELKDNILVSG 430
QY      487 AYDGKIKWDLVVALDPRAPAGTLCRLTV---EHSGRVFLQDFEQIVSSSHDDITLI 543
      431 NADSTVKIWDIKTG-----QCLQTLQGNPKHQAANTVCLQFNKNFVITSSDDGTIVKL 481
QY      544 WD 545
      482 WD 483
DB
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; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-328-877D-10

Query Match      21.1%; Score 640; DB 4; Length 540;
Best Local Similarity 30.8%; Pred. No. 7,2e-59;
Matches 167; Conservative 92; Mismatches 211; Indels 72; Gaps 15;

QY      14 KPNSSEREDCNNGEPKRIPEKNSLRQTNNSCARLCLNQETVCLASTAMKTENCVAKT 73
      4 KLDHSEVRSFSLGKKPCKV-----SEYTSITGL-----VPCSA-----TPTTFGDL 45
      74 KLANGSSMIVPKORKLSASVEKEKL--CVKYEQMSSESDQVEFVHLISQMGHYOHGH 131
      46 RAANGOG-----QQRRIITSVQPTGLOEMLMFQSWGPEKLLADBELIDSCPTQYKH 100
QY      132 INSYLKPMLOPDRFTALPARGLDHAENILSYLDAKSLCAAEIVCKEWYRVTSQDMLMKK 191
      101 MMQVIEPQFQDRDFISLSP---KELALVYLSFLEPKDLLQAQTCRYWRIIAEDNLLMRE 156
QY      192 LIEMVRTDSLWRGLAE---RRMGQOYLFKNKPPDGNAPNPSFYRALYFKTIQDIETI 246
      157 KCKE-----EGIDEPFLHKKRK-----VIRKGFHSPWKSAY-----IRQ--HRI 194
QY      247 ESNMRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIMDKNTLECKRIITGH 306
      195 DYNMRGELKSPKV-LKGHDHVITCLQPCGNRIYVSGSDNTILKWSAVTGKCLRTLVGH 253
QY      307 TGSVYLCLOYDERVIITGSSDSITRVWVDNTGEMLNTLIHCEAVLHLRFNNGMMVTCSKD 366
      254 TGVWSSQMRDNIILISGSTDRTLKVMNAETGECIHTLVGHTSTVACMHLHEKRVVSGRD 313
QY      367 RSIWVMDASPTDITTLRVLVGHRAAVNVDPDDKIVYSASGDTIKVMNTSTGEFRTL 426
      314 ATLRWDIETGQCL---HVLMGHVAARVCQYDGRVVSAGAYDFWVKWDPETETCLHTL 370
QY      427 NGHKRGIACTLOYRDLVWSSGSDNTIRLMDIEGACLRVLEGHELVLCIRFDNKRIVSG 486
      371 QGHTNRVYSLQPDGIHVVSGLDTSIRWVDVETGNCIHTLTHGSLTSGMELKDNILVSG 430
QY      487 AYDGKIKWDLVVALDPRAPAGTLCRLTV---EHSGRVFLQDFEQIVSSSHDDITLI 543
      431 NADSTVKIWDIKTG-----QCLQTLQGNPKHQAANTVCLQFNKNFVITSSDDGTIVKL 481
QY      544 WD 545
      482 WD 483
DB

RESULT 15
US-09-213-888-6
; Sequence 6, Application US/09213888A
; Patent No. 6638731
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Li, Jinhe
; APPLICANT: Pauley, Adele M.
; APPLICANT: Pharmacia & Upjohn Company
; TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
; FILE REFERENCE: 6142
; CURRENT APPLICATION NUMBER: US/09/213,888A
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 6
; LENGTH: 545
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-213-888-6

Query Match      21.1%; Score 640; DB 4; Length 545;
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Best Local Similarity 30.8%; Pred. No. 7.4e-59;
Matches 167; Conservative 92; Mismatches 211; Indels 72; Gaps 15;

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   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 9 KLDHGSERFSFSLGKKPKRV-----SEYSTTGL-----VPCSA-----TPTFGDL 50

QY 74 KLANGTSMTVPKORKLASAYEKEL--CVKYPEQMSSEDOVEFEHLISQWCHYQGH 131
   : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 51 RAANGG-----QQRRTSVQPTGLQEMLKMFQSMGPEKILADELIDSCPTQVKA 105

QY 132 INSYLKPMLOPFTALPARGLDHAENILSYLDAKSLCAELVCKEYRVTSDGMLMK 191
   : : : | | | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 106 RMQVIEPQFQRPDSILLP-----KELALVYSLFLEPKDLQAQTCRYWRIIAEDNLMRE 161

QY 192 LIERWRTDSLWRGLAE-----RCMGQYLFRKKKPPDGNAFPNSFYRALYPKIIDIETI 246
   : : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 162 KCKE-----EGIDEPHIKRRK-----VTKPGFIHSPWKSAY-----IRQ--HRI 199

QY 247 ESNMRCGRHSIORIHCRSETSKGVYCLQYDDOKIVSGLRDNTIKIMDKNTLECKRIITGH 306
   : : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 200 DTNMRGELKSPKV-LKGHDDHVITCLQFCGNRIYSGSDNTLUKWSAVTGKCLRTLVGH 258

QY 307 TGSVLCLOYDERVIITGSSDSTVRVWDVNTGEMLNTLIHCEAVLHLRPNNGMYTCSKD 366
   | | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 259 TCGVWSSQWRDNIIISGSTDRTLKWNNAETGECIHTLYGHTSVRCMHLHEKRVVSGSRD 318

QY 367 RSIATWDMASPTDITLRRLVGVHRAAVNVYDFDDKIYASGDRTIKWNNTSTCEFRVTL 426
   : : | | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 319 ATLRYWDIETGOCL--HYLMGHVAARCVQYDGRVVS GAYDFMWKWDPETETCLHTL 375

QY 427 NGHKGIACTOYRDLRVVSGSSDNTIRLMDICGACLRVLBGHEELVRCIRPDNKRIYSG 486
   | | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 376 QCHTRRVYSLQPDGIHVSGSLDTSIRVWDETGNCHITLTGHQSLTSGMELKDNILVSG 435

QY 487 AYDGKIKWDLVAALDPRAPAGTLCRLTV--EHSGRVYRLQDFEQIVSSSHDITLI 543
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Db 436 NADSTVKIWDIKTG-----QCLQTLQGNPKHQS AVTCLQFNKNFVITSSDGTIVKL 486

QY 544 WD 545
   | |
Db 487 WD 488
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Job time : 27 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 25, 2005, 16:16:36 ; Search time 134 Seconds
(without alignments)
1413.120 Million cell updates/sec

Title: US-09-415-795-4
Perfect score: 3034
Sequence: 1 MDPAAVIOEQKALFKFMNSSE.....PAAQAEPPRSPTTYTISR 569

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1424015 seqs, 332791073 residues

Total number of hits satisfying chosen parameters: 1424015

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	3034	100.0	569	US-10-042-417-2	Sequence 2, Appli
3	3034	100.0	569	US-10-038-010-8	Sequence 8, Appli
4	3034	100.0	569	US-10-652-928-2	Sequence 2, Appli
5	2997	98.8	569	US-10-687-732-18	Sequence 18, Appli
6	2384.5	78.6	542	US-09-832-161-16	Sequence 16, Appli
7	2181	71.9	408	US-10-687-732-15	Sequence 15, Appli
8	1857.5	61.2	407	US-10-687-732-14	Sequence 14, Appli
9	1635.5	53.9	701	US-10-369-493-5420	Sequence 5420, Ap
10	1530	50.4	424	US-10-687-732-13	Sequence 13, Appli
11	1163	33.3	219	US-10-023-530-2	Sequence 2, Appli
12	989.5	32.6	265	US-09-764-848-30	Sequence 30, Appli
13	989.5	32.6	265	US-10-116-016-30	Sequence 30, Appli

14	989.5	32.6	265	14	US-10-222-020-30	Sequence 30, Appli
15	644.5	21.2	626	9	US-09-213-888-21	Sequence 21, Appli
16	644.5	21.2	626	9	US-09-328-877A-21	Sequence 21, Appli
17	644.5	21.2	626	16	US-10-653-497-21	Sequence 21, Appli
18	644.5	21.2	626	16	US-10-653-517-21	Sequence 21, Appli
19	644.5	21.2	626	16	US-10-653-496A-21	Sequence 21, Appli
20	640	21.1	540	9	US-09-213-888-7	Sequence 7, Appli
21	640	21.1	540	9	US-09-213-888-10	Sequence 10, Appli
22	640	21.1	540	9	US-09-328-877A-7	Sequence 7, Appli
23	640	21.1	540	9	US-09-328-877A-10	Sequence 10, Appli
24	640	21.1	540	14	US-10-245-618-14	Sequence 14, Appli
25	640	21.1	540	16	US-10-653-497-7	Sequence 7, Appli
26	640	21.1	540	16	US-10-653-497-10	Sequence 10, Appli
27	640	21.1	540	16	US-10-653-517-7	Sequence 7, Appli
28	640	21.1	540	16	US-10-653-517-10	Sequence 10, Appli
29	640	21.1	540	16	US-10-653-496A-7	Sequence 7, Appli
30	640	21.1	540	16	US-10-653-496A-10	Sequence 10, Appli
31	640	21.1	545	9	US-09-213-888-6	Sequence 6, Appli
32	640	21.1	545	9	US-09-328-877A-6	Sequence 6, Appli
33	640	21.1	545	16	US-10-653-497-6	Sequence 6, Appli
34	640	21.1	545	16	US-10-653-517-6	Sequence 6, Appli
35	640	21.1	545	16	US-10-653-496A-6	Sequence 6, Appli
36	640	21.1	553	9	US-09-213-888-5	Sequence 5, Appli
37	640	21.1	553	9	US-09-328-877A-5	Sequence 5, Appli
38	640	21.1	553	14	US-10-245-618-8	Sequence 8, Appli
39	640	21.1	553	16	US-10-653-497-5	Sequence 5, Appli
40	640	21.1	553	16	US-10-653-517-5	Sequence 5, Appli
41	640	21.1	553	16	US-10-653-496A-5	Sequence 5, Appli
42	640	21.1	559	9	US-09-213-888-9	Sequence 9, Appli
43	640	21.1	559	9	US-09-328-877A-9	Sequence 9, Appli
44	640	21.1	559	16	US-10-653-497-9	Sequence 9, Appli
45	640	21.1	559	16	US-10-653-517-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-09-832-161-18
; Sequence 18, Application US/09832161
; Publication No. US20030166587A1
; GENERAL INFORMATION:
; APPLICANT: Manning, Anthony M.
; APPLICANT: Mercurio, Frank
; APPLICANT: Amic, Sharon
; APPLICANT: Ben-Neriah, Yinnon
; APPLICANT: Davis, Matti
; APPLICANT: Hatzubai, Ada
; APPLICANT: Lavon, Itis
; APPLICANT: Yaron, Avraham
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING ACTIVATION OF
; TITLE OF INVENTION: NF-KB
; FILE REFERENCE: 860098.427
; CURRENT APPLICATION NUMBER: US/09/832,161
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/210,060
; PRIOR FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-832-161-18

Query Match 100.0%; Score 3034; DB 10; Length 569;
Best Local Similarity 100.0%; Pred. No. 8.5e-270;
Matches 569; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPAAVIOEQKALFKFMNSSEEDCNGBPPKIIIPKNSLPQTNISCARLCLINQSTVCLA 60
DB 1 MDPAAVIOEQKALFKFMNSSEEDCNGBPPKIIIPKNSLPQTNISCARLCLINQSTVCLA 60

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QY 61 STAMKTENCVAKTKLANGTSSMIVPKORKLSASYEKEKELCVKFEQMSSEDOVEFVHL 120
DB 61 STAMKTENCVAKTKLANGTSSMIVPKORKLSASYEKEKELCVKFEQMSSEDOVEFVHL 120
QY 121 ISOMCHYOHGHINSYLYKPMLOPDTTALPARGLDHIHENIISYLDKSLCAAEIVCKEMY 180
DB 121 ISOMCHYOHGHINSYLYKPMLOPDTTALPARGLDHIHENIISYLDKSLCAAEIVCKEMY 180
QY 181 RVTSDGMLMKKLIERMVTRTSLMRGLAERRGQYLFKNKPPDGNAPNPSFYRALYPKII 240
DB 181 RVTSDGMLMKKLIERMVTRTSLMRGLAERRGQYLFKNKPPDGNAPNPSFYRALYPKII 240
QY 241 ODIEETIESNMRGCRHSIORIHCRSETSKGVYCLQYDDOKIVSGLRDNTIKIMDKNTLECK 300
DB 241 ODIEETIESNMRGCRHSIORIHCRSETSKGVYCLQYDDOKIVSGLRDNTIKIMDKNTLECK 300
QY 301 RILGHTGSVLCLOYDERVITITGSSDSTVRVWDVNTGEMLNTLIHCEAVLHLRFNNGM 360
DB 301 RILGHTGSVLCLOYDERVITITGSSDSTVRVWDVNTGEMLNTLIHCEAVLHLRFNNGM 360
QY 361 VTCSKDRSIAVWDMASTPDTITLRVLYGHRBAVNVVDFDDKIYASAGDRITIKVWNTSTC 420
DB 361 VTCSKDRSIAVWDMASTPDTITLRVLYGHRBAVNVVDFDDKIYASAGDRITIKVWNTSTC 420
QY 421 EFVRTLNGHKRGIAQLQYRDLVVGSSDNTIRLMDIECGACLRVLEGBHEELVRCIRFDN 480
DB 421 EFVRTLNGHKRGIAQLQYRDLVVGSSDNTIRLMDIECGACLRVLEGBHEELVRCIRFDN 480
QY 481 KRIVSAGYDGKIKWMDLVAALDPRAAGTLCRLTVESGRVRLQDFEQIVSSSHDT 540
DB 481 KRIVSAGYDGKIKWMDLVAALDPRAAGTLCRLTVESGRVRLQDFEQIVSSSHDT 540
QY 541 ILIMDFLNDPAAQAEPPRSPRTTYISR 569
DB 541 ILIMDFLNDPAAQAEPPRSPRTTYISR 569

RESULT 2
US-10-042-417-2
; Sequence 2, Application US/10042417
; Publication No. US20020123082A1
; GENERAL INFORMATION:
; APPLICANT: Pagano, M.
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF
; FILE REFERENCE: 5914-090-999
; CURRENT APPLICATION NUMBER: US/10/042,417
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,179
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-042-417-2

Query Match 100.0%; Score 3034; DB 13; Length 569;
Best Local Similarity 100.0%; Pred. No. 8.5e-270;
Matches 569; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPAAVLQEKALKFNMSSEREDNCNGEPPRKIIPEKNSLRQTYNSCARCLINQETVCLA 60
DB 1 MDPAAVLQEKALKFNMSSEREDNCNGEPPRKIIPEKNSLRQTYNSCARCLINQETVCLA 60
QY 61 STAMKTENCVAKTKLANGTSSMIVPKORKLSASYEKEKELCVKFEQMSSEDOVEFVHL 120
DB 61 STAMKTENCVAKTKLANGTSSMIVPKORKLSASYEKEKELCVKFEQMSSEDOVEFVHL 120
QY 121 ISOMCHYOHGHINSYLYKPMLOPDTTALPARGLDHIHENIISYLDKSLCAAEIVCKEMY 180
DB 121 ISOMCHYOHGHINSYLYKPMLOPDTTALPARGLDHIHENIISYLDKSLCAAEIVCKEMY 180
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QY 181 RVTSDGMLMKKLIERMVTRTSLMRGLAERRGQYLFKNKPPDGNAPNPSFYRALYPKII 240
DB 181 RVTSDGMLMKKLIERMVTRTSLMRGLAERRGQYLFKNKPPDGNAPNPSFYRALYPKII 240
QY 241 ODIEETIESNMRGCRHSIORIHCRSETSKGVYCLQYDDOKIVSGLRDNTIKIMDKNTLECK 300
DB 241 ODIEETIESNMRGCRHSIORIHCRSETSKGVYCLQYDDOKIVSGLRDNTIKIMDKNTLECK 300
QY 301 RILGHTGSVLCLOYDERVITITGSSDSTVRVWDVNTGEMLNTLIHCEAVLHLRFNNGM 360
DB 301 RILGHTGSVLCLOYDERVITITGSSDSTVRVWDVNTGEMLNTLIHCEAVLHLRFNNGM 360
QY 361 VTCSKDRSIAVWDMASTPDTITLRVLYGHRBAVNVVDFDDKIYASAGDRITIKVWNTSTC 420
DB 361 VTCSKDRSIAVWDMASTPDTITLRVLYGHRBAVNVVDFDDKIYASAGDRITIKVWNTSTC 420
QY 421 EFVRTLNGHKRGIAQLQYRDLVVGSSDNTIRLMDIECGACLRVLEGBHEELVRCIRFDN 480
DB 421 EFVRTLNGHKRGIAQLQYRDLVVGSSDNTIRLMDIECGACLRVLEGBHEELVRCIRFDN 480
QY 481 KRIVSAGYDGKIKWMDLVAALDPRAAGTLCRLTVESGRVRLQDFEQIVSSSHDT 540
DB 481 KRIVSAGYDGKIKWMDLVAALDPRAAGTLCRLTVESGRVRLQDFEQIVSSSHDT 540
QY 541 ILIMDFLNDPAAQAEPPRSPRTTYISR 569
DB 541 ILIMDFLNDPAAQAEPPRSPRTTYISR 569

RESULT 3
US-10-038-010-8
; Sequence 8, Application US/10038010
; Publication No. US20030040089A1
; GENERAL INFORMATION:
; APPLICANT: HYBRIGENICS
; APPLICANT: Pierref, Legrain
; TITLE OF INVENTION: Protein-protein interactions in adipocyte cells
; FILE REFERENCE: B4767A
; CURRENT APPLICATION NUMBER: US/10/038,010
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US 60/259,377
; PRIOR FILING DATE: 2001-01-02
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: beta-T-CPI
; LOCATION: (1)..(569)
; OTHER INFORMATION:
US-10-038-010-8

Query Match 100.0%; Score 3034; DB 14; Length 569;
Best Local Similarity 100.0%; Pred. No. 8.5e-270;
Matches 569; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPAAVLQEKALKFNMSSEREDNCNGEPPRKIIPEKNSLRQTYNSCARCLINQETVCLA 60
DB 1 MDPAAVLQEKALKFNMSSEREDNCNGEPPRKIIPEKNSLRQTYNSCARCLINQETVCLA 60
QY 61 STAMKTENCVAKTKLANGTSSMIVPKORKLSASYEKEKELCVKFEQMSSEDOVEFVHL 120
DB 61 STAMKTENCVAKTKLANGTSSMIVPKORKLSASYEKEKELCVKFEQMSSEDOVEFVHL 120
QY 121 ISOMCHYOHGHINSYLYKPMLOPDTTALPARGLDHIHENIISYLDKSLCAAEIVCKEMY 180
DB 121 ISOMCHYOHGHINSYLYKPMLOPDTTALPARGLDHIHENIISYLDKSLCAAEIVCKEMY 180
QY 181 RVTSDGMLMKKLIERMVTRTSLMRGLAERRGQYLFKNKPPDGNAPNPSFYRALYPKII 240
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Db 181 RVTSDGMLMKLIERMVRTDSLWRGLAERRGQGYLFKNKPPDGNAPNSFYRALYPKII 240

Qy 241 ODLETESNMRGRSLORIHCRSETSKGVYCLQYDDOKIVSGLRNTTKIMDKXMLECK 300

Db 241 ODLETESNMRGRSLORIHCRSETSKGVYCLQYDDOKIVSGLRNTTKIMDKXMLECK 300

Qy 301 RLITGHTGSVLCLOQDERVIITGSSDSYRVWVDVNTGEMLNTLIHCEAVLHLPFNNGM 360

Db 301 RLITGHTGSVLCLOQDERVIITGSSDSYRVWVDVNTGEMLNTLIHCEAVLHLPFNNGM 360

Qy 361 VTCSKORSIAVWDMASPTDITLRRVLVGHRAAVNVDPDDKXIVSASGDRITIKWNTSTC 420

Db 361 VTCSKORSIAVWDMASPTDITLRRVLVGHRAAVNVDPDDKXIVSASGDRITIKWNTSTC 420

Qy 421 EFVRLTNGHKGACIQYRDLRVVSGSSDNTIRLMDIEGACLRVLEHGEELVRCIRFNN 480

Db 421 EFVRLTNGHKGACIQYRDLRVVSGSSDNTIRLMDIEGACLRVLEHGEELVRCIRFNN 480

Qy 481 KRIVGAYDGKIKWMDLVAAIDPRAPAGTLCRTLVHSGRVFRLQFDEFQIVSSSHDT 540

Db 481 KRIVGAYDGKIKWMDLVAAIDPRAPAGTLCRTLVHSGRVFRLQFDEFQIVSSSHDT 540

Qy 541 ILIWFNDPAAQAEPSPSRRTTYTISR 569

Db 541 ILIWFNDPAAQAEPSPSRRTTYTISR 569

RESULT 4

US-10-652-928-2

Sequence 2, Application US/10652928

Publication No. US20050079558A1

GENERAL INFORMATION:

APPLICANT: Chaur, D.

APPLICANT: Pagano, M.

APPLICANT: Latres, E.

TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS

FILE REFERENCE: 5914-081

CURRENT APPLICATION NUMBER: US/10/652,928

PRIOR FILING DATE: 2003-08-28

PRIOR APPLICATION NUMBER: US/09/385,219A

PRIOR FILING DATE: 1999-08-27

PRIOR APPLICATION NUMBER: 60/098,355

PRIOR FILING DATE: 1998-08-28

PRIOR APPLICATION NUMBER: 60/118,568

PRIOR FILING DATE: 1999-02-03

PRIOR APPLICATION NUMBER: 60/124,449

PRIOR FILING DATE: 1999-03-15

NUMBER OF SEQ ID NOS: 90

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 2

LENGTH: 569

TYPE: PRT

ORGANISM: Homo sapiens

US-10-652-928-2

Query Match 100.0%; Score 3034; DB 17; Length 569;

Best Local Similarity 100.0%; Pred. No. 8.5e-270;

Matches 569; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDPAAVLOEAKLKPMNSEREDCNGGPPRKIIPEKSLRQTYNSCARLCINQETVCL 60

Db 1 MDPAAVLOEAKLKPMNSEREDCNGGPPRKIIPEKSLRQTYNSCARLCINQETVCL 60

Qy 61 STAMKTENCVAATKLANGTSSMIIVKORKLSASYEKEKELCVKYFEQWSESQVEFVHL 120

Db 61 STAMKTENCVAATKLANGTSSMIIVKORKLSASYEKEKELCVKYFEQWSESQVEFVHL 120

Qy 121 ISOMCHYOHGHINSLKPMLOPDTTALPARGLDHAENIISYLDKSLCAAEVLCCKEY 180

Db 121 ISOMCHYOHGHINSLKPMLOPDTTALPARGLDHAENIISYLDKSLCAAEVLCCKEY 180

Qy 181 RVTSDGMLMKLIERMVRTDSLWRGLAERRGQGYLFKNKPPDGNAPNSFYRALYPKII 240

Db 181 RVTSDGMLMKLIERMVRTDSLWRGLAERRGQGYLFKNKPPDGNAPNSFYRALYPKII 240

Qy 241 ODLETESNMRGRSLORIHCRSETSKGVYCLQYDDOKIVSGLRNTTKIMDKXMLECK 300

Db 241 ODLETESNMRGRSLORIHCRSETSKGVYCLQYDDOKIVSGLRNTTKIMDKXMLECK 300

Qy 301 RLITGHTGSVLCLOQDERVIITGSSDSYRVWVDVNTGEMLNTLIHCEAVLHLPFNNGM 360

Db 301 RLITGHTGSVLCLOQDERVIITGSSDSYRVWVDVNTGEMLNTLIHCEAVLHLPFNNGM 360

Qy 361 VTCSKORSIAVWDMASPTDITLRRVLVGHRAAVNVDPDDKXIVSASGDRITIKWNTSTC 420

Db 361 VTCSKORSIAVWDMASPTDITLRRVLVGHRAAVNVDPDDKXIVSASGDRITIKWNTSTC 420

Qy 421 EFVRLTNGHKGACIQYRDLRVVSGSSDNTIRLMDIEGACLRVLEHGEELVRCIRFNN 480

Db 421 EFVRLTNGHKGACIQYRDLRVVSGSSDNTIRLMDIEGACLRVLEHGEELVRCIRFNN 480

Qy 481 KRIVGAYDGKIKWMDLVAAIDPRAPAGTLCRTLVHSGRVFRLQFDEFQIVSSSHDT 540

Db 481 KRIVGAYDGKIKWMDLVAAIDPRAPAGTLCRTLVHSGRVFRLQFDEFQIVSSSHDT 540

Qy 541 ILIWFNDPAAQAEPSPSRRTTYTISR 569

Db 541 ILIWFNDPAAQAEPSPSRRTTYTISR 569

RESULT 5

US-10-687-732-18

Sequence 18, Application US/10687732

Publication No. US20040171074A1

GENERAL INFORMATION:

APPLICANT: Olicky, Stephen

APPLICANT: Sichen, Frank

APPLICANT: Tyers, Mike

APPLICANT: Willems, Andrew

APPLICANT: Tang, Xiaodong

TITLE OF INVENTION: Structures of Substrate Binding Pockets of SCF Complexes

FILE REFERENCE: 14096.34USU1

CURRENT APPLICATION NUMBER: US/10/687,732

PRIOR FILING DATE: 2003-10-17

PRIOR APPLICATION NUMBER: US 60/419,606

PRIOR FILING DATE: 2002-10-17

NUMBER OF SEQ ID NOS: 43

SOFTWARE: Patentin version 3.2

SEQ ID NO 18

LENGTH: 569

TYPE: PRT

ORGANISM: Mus musculus

PUBLICATION INFORMATION:

DATABASE ACCESSION NUMBER: Genbank/NP_033901

DATABASE ENTRY DATE: 1998-08-04

RELEVANT RESIDUES: (1)..(569)

US-10-687-732-18

Query Match 98.8%; Score 2997; DB 16; Length 569;

Best Local Similarity 98.6%; Pred. No. 2.1e-266;

Matches 561; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MDPAAVLOEAKLKPMNSEREDCNGGPPRKIIPEKSLRQTYNSCARLCINQETVCL 60

Db 1 MDPAAVLOEAKLKPMNSEREDCNGGPPRKIIPEKSLRQTYNSCARLCINQETVCL 60

Qy 61 STAMKTENCVAATKLANGTSSMIIVKORKLSASYEKEKELCVKYFEQWSESQVEFVHL 120

Db 61 STAMKTENCVAATKLANGTSSMIIVKORKLSASYEKEKELCVKYFEQWSESQVEFVHL 120

Qy 121 ISOMCHYOHGHINSLKPMLOPDTTALPARGLDHAENIISYLDKSLCAAEVLCCKEY 180

Db 121 ISOMCHYOHGHINSLKPMLOPDTTALPARGLDHAENIISYLDKSLCAAEVLCCKEY 180

Qy 181 RVTSDGMLMKLIERMVRTDSLWRGLAERRGQGYLFKNKPPDGNAPNSFYRALYPKII 240

Db 181 RVTSDGMLWKLIERRVETDLSLWGLAERBGWGYLFKNKPPDENAPNSFYRALYPKII 240
Qy 241 ODIEETIESNMWRCGRHSLSORIHCRSETSKGVYCLQYDDOKIYSGALADNTIKIMDKTSLCK 300
Db 241 ODIEETIESNMWRCGRHSLSORIHCRSETSKGVYCLQYDDOKIYSGALADNTIKIMDKTSLCK 300
Qy 301 RLITGHTGVSVCLOQYDERVIITGSSSDSTYRVWVDVNTGEMANTLIHCEAVLHLPFNNGM 360
Db 301 RLITGHTGVSVCLOQYDERVIITGSSSDSTYRVWVDVNTGEMANTLIHCEAVLHLPFNNGM 360
Qy 361 VTCSKORSIAVWDMASPTDITLRRVLYGHRAAVNVVDPDDKXIYASGDRITIKWNTSTC 420
Db 361 VTCSKORSIAVWDMASPTDITLRRVLYGHRAAVNVVDPDDKXIYASGDRITIKWNTSTC 420
Qy 421 EFWRLTNGHKRGIAQLQYRDRLVVGSSSDNTIRLMDIEGACLRVLEGBEELVRCIRF 480
Db 421 EFWRLTNGHKRGIAQLQYRDRLVVGSSSDNTIRLMDIEGACLRVLEGBEELVRCIRF 480
Qy 481 KRIVGAYDGKIKWDLVAALDPRAPAGTLCRLTVESGRVFRLOPDEFOIVSSSHD 540
Db 481 KRIVGAYDGKIKWDLVAALDPRAPAGTLCRLTVESGRVFRLOPDEFOIVSSSHD 540
Qy 541 IILWDFLNDPAAQAEPSPSRRTTYISR 569
Db 541 IILWDFLNDPAAQAEPSPSRRTTYISR 569

RESULT 6

US-09-832-161-16
; Sequence 16, Application US/09832161
; Publication No. US2003016587A1
; GENERAL INFORMATION:
; APPLICANT: Manning, Anthony M.
; APPLICANT: Mercurio, Frank
; APPLICANT: Amit, Sharon
; APPLICANT: Ben-Neriah, Yimon
; APPLICANT: Davis, Matli
; APPLICANT: Hatzubai, Ada
; APPLICANT: Lavon, Irit
; APPLICANT: Yaron, Avraham
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING ACTIVATION OF
; TITLE OF INVENTION: NF-kB
; FILE REFERENCE: 860098.427
; CURRENT APPLICATION NUMBER: US/09/832,161
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/210,060
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 542
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-832-161-16

Query Match 78.6%; Score 2384.5; DB 10; Length 542;
Best Local Similarity 79.0%; Pred. No. 4.2e-210;
Matches 451; Conservative 48; Mismatches 41; Indels 31; Gaps 7;

Qy 1 MDPAAVLQEKALFKMNSREDNNGBPRKTIPEKNSLRQTYNSCARLCLINQETVCLA 60
Db 1 MDPAAVLQEKALFKMNSREDNNGBPRKTIPEKNSLRQTYNSCARLCLINQETVCLA 60
Qy 61 S--TAMKTNCVAKTKYLANGTSMIVPKORKLASAYEKEKELCVKFFQWSSSDOVEFE 118
Db 61 S--TAMKTNCVAKTKYLANGTSMIVPKORKLASAYEKEKELCVKFFQWSSSDOVEFE 118
Qy 37 SCLQSPVYRCL--QISNGTSSVIVSRKRPSEBGNVQKEXKDLCKYFQDMSESDDVEFE 93
Db 37 SCLQSPVYRCL--QISNGTSSVIVSRKRPSEBGNVQKEXKDLCKYFQDMSESDDVEFE 93
Qy 119 HLISQCHQOHGHINSYKPKMLQRPDITLPAKGLDHTAENTLSYDAKSLCAALYCKE 178
Db 94 HLISQCHQOHGHINSYKPKMLQRPDITLPAKGLDHTAENTLSYDAKSLCAALYCKE 153
Qy 179 WYRVTSDDGMLWKLIERRVETDLSLWGLAERBGWGYLFKNKPPDENAPNSFYRALYPK 238
Db 179 WYRVTSDDGMLWKLIERRVETDLSLWGLAERBGWGYLFKNKPPDENAPNSFYRALYPK 238

Db 154 WQVISEGMLWKLIERRVETDPLMKGLSRRGWGYLFKNRPTDG--PNSFYRSLYPK 211
Qy 239 IIOIEETIESNMWRCGRHSLSORIHCRSETSKGVYCLQYDDOKIYSGALADNTIKIMDKTSLCK 298
Db 212 IIOIEETIESNMWRCGRHSLSORIHCRSETSKGVYCLQYDDOKIYSGALADNTIKIMDKTSLCK 271
Qy 299 CKRLITGHTGVSVCLOQYDERVIITGSSSDSTYRVWVDVNTGEMANTLIHCEAVLHLPFNNG 358
Db 272 CKRLITGHTGVSVCLOQYDERVIITGSSSDSTYRVWVDVNTGEMANTLIHCEAVLHLPFNNG 331
Qy 359 MMTVCSKORSIAVWDMASPTDITLRRVLYGHRAAVNVVDPDDKXIYASGDRITIKWNTSTC 418
Db 332 LMVCSKORSIAVWDMASPTDITLRRVLYGHRAAVNVVDPDDKXIYASGDRITIKWNTSTC 391
Qy 419 TCEFWRLTNGHKRGIAQLQYRDRLVVGSSSDNTIRLMDIEGACLRVLEGBEELVRCIRF 478
Db 392 TCEFWRLTNGHKRGIAQLQYRDRLVVGSSSDNTIRLMDIEGACLRVLEGBEELVRCIRF 451
Qy 479 DNKRIVGAYDGKIKWDLVAALDPRAPAGTLCRLTVESGRVFRLOPDEFOIVSSSHD 538
Db 452 DNKRIVGAYDGKIKWDLVAALDPRAPAGTLCRLTVESGRVFRLOPDEFOIVSSSHD 511
Qy 539 DTLIWDPLNDPAAQAEPSPSRRTTYISR 569
Db 512 DTLIWDPLNDPAAQAEPSPSRRTTYISR 542

RESULT 7

US-10-687-732-15
; Sequence 15, Application US/10687732
; Publication No. US2004017107A1
; GENERAL INFORMATION:
; APPLICANT: Orlicky, Stephen
; APPLICANT: Siebert, Frank
; APPLICANT: Tyers, Mike
; APPLICANT: Williams, Andrew
; APPLICANT: Tang, Xiaojing
; TITLE OF INVENTION: Structures of Substrate Binding Pockets of SCF Complexes
; FILE REFERENCE: 14096.34USU1
; CURRENT APPLICATION NUMBER: US/10/687,732
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: US 60/419,606
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 408
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-687-732-15

Query Match 71.9%; Score 2181; DB 16; Length 408;
Best Local Similarity 100.0%; Pred. No. 1.4e-191;
Matches 408; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 140 LQRPDITLPAKGLDHTAENTLSYDAKSLCAALYCKEWTYRVSDGMLWKLIERRV 199
Db 1 LQRPDITLPAKGLDHTAENTLSYDAKSLCAALYCKEWTYRVSDGMLWKLIERRV 60
Qy 200 DSLWGLAERBGWGYLFKNKPPDENAPNSFYRALYPKIIODIEETIESNMWRCGRHSLSOR 259
Db 61 DSLWGLAERBGWGYLFKNKPPDENAPNSFYRALYPKIIODIEETIESNMWRCGRHSLSOR 120
Qy 260 IHCRSETSKGVYCLQYDDOKIYSGALADNTIKIMDKTSLCKRLITGHTGVSVCLOQYDERV 319
Db 121 IHCRSETSKGVYCLQYDDOKIYSGALADNTIKIMDKTSLCKRLITGHTGVSVCLOQYDERV 180
Qy 320 IITSSSDSTYRVWVDVNTGEMANTLIHCEAVLHLPFNNGMMVTSKORSIAVWDMASPTD 379
Db 181 IITSSSDSTYRVWVDVNTGEMANTLIHCEAVLHLPFNNGMMVTSKORSIAVWDMASPTD 240
Qy 380 IILRRVLYGHRAAVNVVDPDDKXIYASGDRITIKWNTSTCEFWRLTNGHKRGIAQLQYR 439
Db 380 IILRRVLYGHRAAVNVVDPDDKXIYASGDRITIKWNTSTCEFWRLTNGHKRGIAQLQYR 439

Db 241 ITLRVLVGHRAAVNVVDEDDKXIYASAGDRTIKWNTSTCEFRVLTNGHKGIAQLQYR 300
QY 440 DLVYVSGSSDNTIRLMDIEGACLRLEGEHELVRICIRPDNRKIYSGADGKIYWDVLA 499
Db 301 DLVYVSGSSDNTIRLMDIEGACLRLEGEHELVRICIRPDNRKIYSGADGKIYWDVLA 360
QY 500 ALDPRAPAGTLCRLTVESHSGRVFLQDPFQIVSSSHDDTILIMDFL 547
Db 361 ALDPRAPAGTLCRLTVESHSGRVFLQDPFQIVSSSHDDTILIMDFL 408

RESULT 8

US-10-687-732-14
; Sequence 14, Application US/10687732
; Publication No. US20040171074A1
; GENERAL INFORMATION:
; APPLICANT: Orlicky, Stephen
; APPLICANT: Slicherl, Frank
; APPLICANT: Tyers, Mike
; APPLICANT: Willems, Andrew
; APPLICANT: Tang, Xiaojing
; TITLE OF INVENTION: Structures of Substrate Binding Pockets of SCF Complexes
; FILE REFERENCE: 14096.34US01
; CURRENT APPLICATION NUMBER: US/10/687,732
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: US 60/419,606
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 407
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-687-732-14

Query Match 61.2%; Score 1857.5; DB 16; Length 407;
Best Local Similarity 85.0%; Pred. No. 8.1e-162;
Matches 347; Conservative 30; Mismatches 30; Indels 1; Gaps 1;

QY 140 LORDITLTPARGLDHIAENILSYDPAKSLCAELVCKEWRVYSDGMLMKLIERMVT 199
Db 1 LORDITLTPARGLDHIAENILSYDPAKSLCAELVCKEWRVYSDGMLMKLIERMVT 60
QY 200 DSLMGLAERRGMGOYLFPKRPDPDGNAPNSFYRALYPKIIDIERIESNMRGSHLOR 259
Db 61 DSLMGLAERRGMGOYLFPKRPDPDGNAPNSFYRALYPKIIDIERIESNMRGSHLOR 119
QY 260 IHCRESYSGVYCLQYDDQKIVSGLRDNTIKIMDKNLTCEKRILNGHTGSVLCQYDERV 319
Db 120 INCRENSGVCYCLQYDDQKIVSGLRDNTIKIMDKNLTCEKRILNGHTGSVLCQYDDQV 179
QY 320 IITGSSDSSTVRVWVDVNTGEMNTLIIHCEAVLHLRPNNGMVTCSKDRSIAVWMAASPTD 379
Db 180 IITGSSDSSTVRVWVDVNTGEMNTLIIHCEAVLHLRPNNGMVTCSKDRSIAVWMAASPTD 239
QY 380 ITLRVLVGHRAAVNVVDDDKXIYASAGDRTIKWNTSTCEFRVLTNGHKGIAQLQYR 439
Db 240 ITLRVLVGHRAAVNVVDDDKXIYASAGDRTIKWNTSTCEFRVLTNGHKGIAQLQYR 299
QY 440 DLVYVSGSSDNTIRLMDIEGACLRLEGEHELVRICIRPDNRKIYSGADGKIYWDVLA 499
Db 300 DLVYVSGSSDNTIRLMDIEGACLRLEGEHELVRICIRPDNRKIYSGADGKIYWDVLA 359
QY 500 ALDPRAPAGTLCRLTVESHSGRVFLQDPFQIVSSSHDDTILIMDFL 547
Db 360 ALDPRAPAGTLCRLTVESHSGRVFLQDPFQIVSSSHDDTILIMDFL 407

RESULT 9
US-10-369-493-5420
; Sequence 5420, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Tyers, Mike
; APPLICANT: Willems, Andrew

; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 5420
; LENGTH: 701
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-5420

Query Match 53.9%; Score 1635.5; DB 15; Length 701;
Best Local Similarity 57.7%; Pred. No. 4.6e-141;
Matches 328; Conservative 69; Mismatches 116; Indels 55; Gaps 8;

QY 31 RKIPEKXSLRQTVNSCARLCINQETVCLASTAMKTENCVAKTXLN-----GTS 80
Db 2 RRFREGKALKRGARADGSGIQLATVCST-----IERCF--TAVSNPIFLPSTPFSVF 55
QY 81 SMIVPKQR---KLASVEKEKELCVKYPFQWSSDDQVEVHLISQCHYQHGHINSY 135
Db 56 SFLPSPRMTQIFLVSRSFSFSFSEVL-----KMSHEQLDFMDKIVHRLSHYOLGVDFNF 110
QY 136 LKPMLODPITLTPARGLDHIAENILSYDPAKSLCAELVCKEWRVYSDGMLMKLIER 195
Db 111 IRPMLQDPISMLP---HLVELILFVNVSLSLCSBVSSTWRCALARQGMWKKLIER 166
QY 236 YPKIIOIETTESNMRGSHLQRIHCRSEYSGVYCLQYDDQKIVSGLRDNTIKIMDKN 295
Db 227 YPKIIRIDHINIDNMKRGVYKMTIRINQSENSKGYVCLQYDDQKIVSGLRDNTIKIMDKN 286
QY 236 TLECRRIITGHTGSLVCLQYDERVITGSSDSSTVRVWVDVNTGEMNTLIIHCEAVLHLRF 355
Db 287 DYSCSRILISGHTGSLVCLQYDNRVITGSSDSSTVRVWVDVNTGEMNTLIIHCEAVLHLRF 346
QY 356 NNGMNVTSKDRSIAVWMAASPTDITLRLVVLVGHRAAVNVVDDDKXIYASAGDRTIKW 415
Db 347 ANGINVTSKDRSIAVWMAASPTDITLRLVVLVGHRAAVNVVDDDKXIYASAGDRTIKW 406
QY 416 NTSTCEFRVLTNGHKGIAQLQYDRDLVYVSGSSDNTIRLMDIEGACLRLEGEHELVRIC 475
Db 407 SMDTLLEFRVLTNGHKGIAQLQYDRDLVYVSGSSDNTIRLMDIEGACLRLEGEHELVRIC 466
QY 476 IRFDNRKIVSAGYDGIKIVWDLVLAALDPRAPAGTLCRLTVESHSGRVFLQDPFQIVSS 535
Db 467 IRFDNRKIVSAGYDGIKIVWDLVLAALDPRAPAGTLCRLTVESHSGRVFLQDPFQIVSS 526
QY 536 SHDDTILIMDFLNDPAAQAEPPRSPRT 563
Db 527 SHDDTILIMDFLNDPAAQAEPPRSPRT 549

RESULT 10
US-10-687-732-13
; Sequence 13, Application US/10687732
; Publication No. US20040171074A1
; GENERAL INFORMATION:
; APPLICANT: Orlicky, Stephen
; APPLICANT: Slicherl, Frank
; APPLICANT: Tyers, Mike
; APPLICANT: Willems, Andrew

```
APPLICANT: Tang, Xiaojing
TITLE OF INVENTION: Structures of Substrate Binding Pockets of SCR Complexes
FILE REFERENCE: 14096.34USU1
CURRENT APPLICATION NUMBER: US/10/667,732
CURRENT FILING DATE: 2003-10-17
PRIOR APPLICATION NUMBER: US 60/419,606
PRIOR FILING DATE: 2002-10-17
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn version 3.2
SEQ ID NO 13
LENGTH: 424
TYPE: PRT
ORGANISM: Caenorhabditis elegans
US-10-667-732-13

Query Match
Best Local Similarity 50.4%; Score 1530; DB 16; Length 424;
Matches 296; Conservative 38; Mismatches 70; Indels 24; Gaps 2;

QY 140 LORDFTLPAAGLDHIAENITSLYDAKSLCAELVCKEYRVTSDDGLMKLIERMRT 199
DB 1 LORDFTSLMPPA---HLVELILFVNVSLSKSCSEVSTSMRCALARGHMKKLEKNVRS 56
QY 200 DLMWGLAERGMGQYL-----FKNKPPDGNAPNSFYRALYFKI 239
DB 57 DLMWGLSEKRGMDKFLNISRDMSVRI CEKNFYDVNI KRDQLDGLIMHVFYSKLYPKI 116
QY 240 IODIETISNMRGSHSLQRIHCRSETSKGYVCLQYDDQKIVSGIRDNTIKIWDKNTLBC 299
DB 117 IRDINHNNMMKRGYKMTIRINCOSENSKGYVCLQYDDDKIVSGIRDNTIKIWDKNSC 176
QY 300 KRILGHGHSYVCLQYDERVITTSDDSTVRVWDVNTGEMNTLTHHCEAVLHLPFNNGM 359
DB 177 SRIISGHTSGYVCLQYDRKVVIISSGSDATVRVWDVETGCTITLHHCBAVLHLPFNGI 236
QY 360 MWTGSKDRSIAVMDNASPTDITLRVLVGHRAAVNVVFPDDKYIVSASGDRTIKYWNTST 419
DB 237 MWTGSKDRSIAVMDVSPRDIIRVVLVGHRAAVNVVFPDDKYIVSASGDRTIKYWMDT 296
QY 420 CEFVTLNGHKRGICLQYRDLVVGSSDNTIRIMDIECGALCVLBSGHELVLCIRPD 479
DB 297 LEFVTLNGHRRGICLQYRGRLVVGSSSDNTIRIMDISHGCVLVLBSGHELVLCIRPD 356
QY 480 NKRIYSGAYDGIKIVMDIQAALDPRAPAGTLCRLTVLHSGVRFLOPDEQIVSSHDD 539
DB 357 EKRIYSGAYDGIKIVMDIQAALDPRALSEIICLCLVQHTGKRVFLQFPDIYSSSHD 416
QY 540 TILIMDFL 547
DB 417 TILIMDFL 424

RESULT 11
US-10-023-530-2
; Sequence 2, Application US/10023530
; Publication No. US20030007956A1
; GENERAL INFORMATION:
; APPLICANT: LEGRAIN, Pierre
; APPLICANT: BENAROUS, Richard
; APPLICANT: BLOT, Guillaume
; APPLICANT: LASSOT, Irina
; TITLE OF INVENTION: PROTEINS THAT INTERACT WITH BETA TROP
; FILE REFERENCE: B4717A
; CURRENT APPLICATION NUMBER: US/10/023,530
; CURRENT FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: 60/256,276
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
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FEATURE:
; NAME/KEY: BetaTrop
; LOCATION: (1)..(219)
; OTHER INFORMATION: F-box protein
US-10-023-530-2

Query Match
Best Local Similarity 38.3%; Score 1163; DB 14; Length 219;
Matches 219; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPAAVLQEKALFKMNSEREDCNNGEPKKIIPKNSLRQTYNSCARLCLNQETVCLA 60
DB 1 MDPAAVLQEKALFKMNSEREDCNNGEPKKIIPKNSLRQTYNSCARLCLNQETVCLA 60
QY 61 STAKTENCVAKTGLANGTSMIVPKRKLSASYEKEKELCVKFEQMSSEDQVEFVHL 120
DB 61 STAKTENCVAKTGLANGTSMIVPKRKLSASYEKEKELCVKFEQMSSEDQVEFVHL 120
QY 121 ISOMCHYOHGHINSYLPMLORDFTLPAAGLDHIAENITSLYDAKSLCAELVCKEY 180
DB 121 ISOMCHYOHGHINSYLPMLORDFTLPAAGLDHIAENITSLYDAKSLCAELVCKEY 180
QY 181 RVTSDGMLMKKLIBRMVRTDLSLWGLAERGMGQYLFKN 219
DB 181 RVTSDGMLMKKLIBRMVRTDLSLWGLAERGMGQYLFKN 219

RESULT 12
US-09-764-848-30
; Sequence 30, Application US/09764848
; Patent No. US20020077270A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT208
; CURRENT APPLICATION NUMBER: US/09/764,848
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PAM or file wrapper
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-848-30

Query Match
Best Local Similarity 32.6%; Score 989.5; DB 9; Length 265;
Matches 186; Conservative 24; Mismatches 21; Indels 39; Gaps 3;

QY 15 FMNSEREDCNNGEPKKIIPKNSLRQTYNSCARLCLNQETVCLASTAKTENCVAKT 74
DB 20 FMNSEREDCNNGEPKKIIPKNSLRQTYNSCARLCLNQETVCLASTAKTENCVAKT 74
QY 75 LANGTSMIVPKRKLSASYEKEKELCVKFEQMSSEDQVEFVHLISOMCHYOHGHINS 134
DB 43 ISNGTSSIVYSRKRPSEGNVYKEKDLCTKTFDDQSESDQVEFVHLISRMCHYOHGHINS 102
QY 135 YLKPMLOPFTLPAAGLDHIAENITSLYDAKSLCAELVCKEYRVTSDDGLMKLIE 194
DB 103 YLKPMLOPFTLPAAGLDHIAENITSLYDARSLCAELVCKEYRVTSDDGLMKLIE 162
QY 195 RMVRTDLSLWGLAERGMGQYLFKNKPPDGNAPNSFYRALYPKIIDIETISNMRGR 254
DB 163 RMVRTDLSLWGLAERGMGQYLFKNRPPDG--PNNSFYRLYPKIIDIETISNMRGR 220
QY 255 HSLQRIHCRSETSKGYVCLQYDDQKIVSGL 284
DB 221 HNLQRIQCRSENSKGYVCLQYDDKIVSGL 250

RESULT 13
US-10-116-016-30
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```
; Sequence 30, Application US/10116016
; Publication No. US20030054379A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT208C1
; CURRENT APPLICATION NUMBER: US/10/116,016
; CURRENT FILING DATE: 2002-04-05
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 30
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-116-016-30

Query Match      32.6%; Score 989.5; DB 14; Length 265;
Best Local Similarity 68.9%; Pred. No. 2.9e-82;
Matches 186; Conservative 24; Mismatches 21; Indels 39; Gaps 3;

QY      15  FMNSEREDCNNGEPPRKTIPEKNSLRQTTNSCARLCLNQETVCLASTAMKTENCVAATK 74
      20  FQNTSVMEQNDDESPK-----KNTLWQ-----
      75  LANGSSMTVPKQKRLASYEKEKELCVKYEFEWSEDOVEFEHLISQMCHYOHGHINS 134
      43  ISNGSVSVSVSRKRSEGVYQKEKDLCKYFQWSESDQVEFEHLISMCYOHGHINS 102
QY      135  YKPMLODFITLALPARGLDHAENILSYLDAKSLCAELVCKEWRYVTSQMLMKKLE 194
      103  YKPMLODFITLALPEQGDHAENILSYLDAKSLCAELVCKEWRYVTSQMLMKKLE 162
QY      195  RMVRTDSLMLRGLAERGMQYIFKPKPPDGNAPPNVSFYRALYPKTIIDITETESWRCGR 254
      163  RMVRTDPLMKGLSERGMQYIFKPKPDTG--PPNSFYSLYPKTIIDITETESWRCGR 220
QY      255  HSLOHCRSETSKGVYCYQYDOKIVSGT 284
      221  HMLQRIQCRSENSKGVYCYQYDOKIVSGT 250
Db

RESULT 14
US-10-222-020-30
; Sequence 30, Application US/10222020
; Publication No. US20030175739A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT208C2
; CURRENT APPLICATION NUMBER: US/10/222,020
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 10/116,016
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 09/764,848
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
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; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/225,757
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/226,868
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/216,647
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,267
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/216,880
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,270
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/251,869
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/235,834
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/234,274
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/234,223
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/228,924
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/224,518
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/236,369
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/224,519
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,964
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/241,809
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/249,299
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/236,327
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/241,785
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/244,617
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 60/225,268
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/236,368
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/251,856
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/251,868
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/229,344
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/234,997
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: 60/229,343
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,345
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,287
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,513
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/231,413
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/229,509
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/236,367
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/237,039
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,038
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/236,370
; PRIOR FILING DATE: 2000-09-29
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;; PRIOR APPLICATION NUMBER: 60/236,802
;; PRIOR FILING DATE: 2000-10-02
;; PRIOR APPLICATION NUMBER: 60/237,037
;; PRIOR FILING DATE: 2000-10-02
;; PRIOR APPLICATION NUMBER: 60/237,040
;; PRIOR FILING DATE: 2000-10-02
;; PRIOR APPLICATION NUMBER: 60/240,960
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/239,935
;; PRIOR FILING DATE: 2000-10-13
;; PRIOR APPLICATION NUMBER: 60/239,937
;; PRIOR FILING DATE: 2000-10-13
;; PRIOR APPLICATION NUMBER: 60/241,787
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/246,474
;; PRIOR FILING DATE: 2000-11-08
;; PRIOR APPLICATION NUMBER: 60/246,532
;; PRIOR FILING DATE: 2000-11-08
;; PRIOR APPLICATION NUMBER: 60/249,216
;; PRIOR FILING DATE: 2000-11-17
;; PRIOR APPLICATION NUMBER: 60/249,210
;; PRIOR FILING DATE: 2000-11-17
;; PRIOR APPLICATION NUMBER: 60/226,681
;; PRIOR FILING DATE: 2000-08-22
;; PRIOR APPLICATION NUMBER: 60/225,759
;; PRIOR FILING DATE: 2000-08-14
;; PRIOR APPLICATION NUMBER: 60/225,213
;; PRIOR FILING DATE: 2000-08-14
;; PRIOR APPLICATION NUMBER: 60/227,182
;; PRIOR FILING DATE: 2000-08-22
;; PRIOR APPLICATION NUMBER: 60/225,214
;; PRIOR FILING DATE: 2000-08-14
;; PRIOR APPLICATION NUMBER: 60/235,836
;; PRIOR FILING DATE: 2000-09-27
;; PRIOR APPLICATION NUMBER: 60/230,438
;; PRIOR FILING DATE: 2000-09-06
;; PRIOR APPLICATION NUMBER: 60/215,135
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: 60/225,266
;; PRIOR FILING DATE: 2000-08-14
;; PRIOR APPLICATION NUMBER: 60/249,218
;; PRIOR FILING DATE: 2000-11-17
;; PRIOR APPLICATION NUMBER: 60/249,208
;; PRIOR FILING DATE: 2000-11-17
;; PRIOR APPLICATION NUMBER: 60/249,213
;; PRIOR FILING DATE: 2000-11-17
;; PRIOR APPLICATION NUMBER: 60/249,212
;; PRIOR FILING DATE: 2000-11-17
;; PRIOR APPLICATION NUMBER: 60/249,207
;; PRIOR FILING DATE: 2000-11-17
;; PRIOR APPLICATION NUMBER: 60/249,245
;; PRIOR FILING DATE: 2000-11-17
;; PRIOR APPLICATION NUMBER: 60/249,244
;; PRIOR FILING DATE: 2000-11-17
;; PRIOR APPLICATION NUMBER: 60/249,217
;; PRIOR FILING DATE: 2000-11-17
;; PRIOR APPLICATION NUMBER: 60/249,211
;; PRIOR FILING DATE: 2000-11-17
;; PRIOR APPLICATION NUMBER: 60/249,215
;; PRIOR FILING DATE: 2000-11-17
;; PRIOR APPLICATION NUMBER: 60/249,264
;; PRIOR FILING DATE: 2000-11-17
;; PRIOR APPLICATION NUMBER: 60/249,214
;; PRIOR FILING DATE: 2000-11-17
;; PRIOR APPLICATION NUMBER: 60/249,297
;; PRIOR FILING DATE: 2000-11-17
;; PRIOR APPLICATION NUMBER: 60/232,400
;; PRIOR FILING DATE: 2000-09-14
;; PRIOR APPLICATION NUMBER: 60/231,242
;; PRIOR FILING DATE: 2000-09-08
;; PRIOR APPLICATION NUMBER: 60/232,081
;; PRIOR FILING DATE: 2000-09-08
;; PRIOR APPLICATION NUMBER: 60/232,080

;; PRIOR FILING DATE: 2000-09-08
;; PRIOR APPLICATION NUMBER: 60/231,414
;; PRIOR FILING DATE: 2000-09-08
;; PRIOR APPLICATION NUMBER: 60/231,244
;; PRIOR FILING DATE: 2000-09-08
;; PRIOR APPLICATION NUMBER: 60/233,064
;; PRIOR FILING DATE: 2000-09-14
;; PRIOR APPLICATION NUMBER: 60/233,063
;; PRIOR FILING DATE: 2000-09-14
;; PRIOR APPLICATION NUMBER: 60/232,397
;; PRIOR FILING DATE: 2000-09-14
;; PRIOR APPLICATION NUMBER: 60/232,399
;; PRIOR FILING DATE: 2000-09-14
;; PRIOR APPLICATION NUMBER: 60/232,401
;; PRIOR FILING DATE: 2000-09-14
;; PRIOR APPLICATION NUMBER: 60/241,808
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/241,826
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/241,786
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/241,221
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/246,475
;; PRIOR FILING DATE: 2000-11-08

Query Match 32.6%; Score 989.5; DB 14; Length 265;

Best Local Similarity 66.9%; Pred. No. 2.9e-82; Matches 186; Conservative 24; Mismatches 21; Indels 39; Gaps 3;

QY 15 FMNSEREDCNGEPKRIPEKNSLRQTNSCARCLINQBTVCIASTAMKTENCVAKTK 74
DB 20 FQNTSWEDQNEDESPK-----KNTLWQ----- 42
QY 75 LANTSSMIVPKQKLSASIEKEKELCVKTFEONSBSDOYEFVHLLISOMCHYGHINS 134
DB 43 ISNTSSVIVSRKRPSSRGNYQKEKDLCKTFDDWSBDQVEFVHLLSRMCHYGHINS 102
QY 135 YLKPMLOPFTLAPAGLHIAENILSYLDASLCAAEIVCKEWRVTSQGMKKLIE 194
DB 103 YLKPMLOPFTLAPAGLHIAENILSYLDASLCAAEIVCKEWRVTSQGMKKLIE 162
QY 195 RMVETDSLMBGLAERMGQYLFKNKPPDGNAPNSFYRALYPIIIDITETESNMRGR 254
DB 163 RMVETDPLMKGLSRMRQDQYLFKNRPTDG--PENSTYRSLYPIIIDITETESNMRGR 220
QY 255 HSLQRIHCRSETSKGVYCLQYDQKIVSGL 284
DB 221 HNLQRIQCRSENSKGVYCLQYDDEKIIISGL 250

RESULT 15

US-09-213-888-21

; Sequence 21, Application US/09213888A

; Patent No. US20020164683A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Li, Jimne

; APPLICANT: Pauley, Adele M.

; TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that

; TITLE OF INVENTION: Encode Them

; FILE REFERENCE: 6142

; CURRENT APPLICATION NUMBER: US/09/213,888A

; CURRENT FILING DATE: 1998-12-17

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 21

; LENGTH: 626

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: 6 myc tagged

OTHER INFORMATION: homo sapien
US-09-213-888-21

Query Match 21.2%; Score 644.5; DB 9; Length 626;

Best Local Similarity 30.1%; Pred. No. 5.3e-50;
Matches 169; Conservative 103; Mismatches 222; Indels 67; Gaps 15;

```

QY      8 LQEKALKFNNSSEREDCNNGEPKRIIPK--NSLRQ--TNSCARLCLNQETVCLASTA 63
DB      53 MEQKLISEEDLNEMESLGLTMBQKLISEEDLNMRKRLDHGSEVRSLGKKPKCVSEY 112
QY      64 MXTENCV-----AKTKLANGTSSMTVPKORKLASYEKEKEP--CVKTFEQWSESD 112
DB      113 TSTTGLVPCSATPTTGGDLRAANGQ-----QQRRTITVQPTTGOEWLKMFGWSGPE 167
QY      113 QVEFEHLISQWCHQOHGINSYKMLORDFITLPAKGLDHIAENIISYLDKSLCA 172
DB      168 KLALDELIDSCPTQVKMMQVIEPQFORDFISLP---KELALYVLSFLEPKDLLQA 223
QY      173 ELVCKEYVAVTSDGMLMKLIERMVRTDLSLWRGLAE---RRGWQYLFKNKPPDGNAP 227
DB      224 AOTCRVWRLADNLMREKCKE-----EGIDELPHIKRK-----VTKPGFIHSP 269
QY      228 PMSFYRALYPKIIDIETIESNMRCGRHSLQRIHGRSETSKGVYCIQYDDQKIVSGLRDN 287
DB      270 WKSAY-----IRQ--HRIDTMRREGELKSPKV-LKGDHDVITCQFGGNRIVSGSDN 320
QY      288 TIKIDKNTLECKRIILTGHTGSVLCIQYDERVIYITGSSDSTVRVMDVNTGEMLNTLIHHC 347
DB      321 TLKWSAVYTGKICRLTVGHTGVWSQMRDNIISGSTDRTLKWNNAETGECIHITLYGHT 380
QY      348 EAVLHLRFNNGMMVYCSKXDSIAVWDMASPTDITLRVLVGHRAVNVVDPEDKYIVSAS 407
DB      381 STVRGMHLHKKRVVSGSRDATTLRVMDIETGQCL--HVLMGHVAARVCVQYDGRRVSGA 437
QY      408 GDRITKVVNTSTCEFRVTLNGHKRGIAQLQYRDLVVGSSSDNTIRLMDIECGACLRVLE 467
DB      438 YDFWYKVMDEPETCTCHTLQGHTRVYSIQFDGIHVSSGLDTSIRVMDVEFGNCIHITLT 497
QY      468 GHEELVRCIRFPNKRIVSGAYDGKIKVMDLVALDPRAPAGTLCRLTV--EHSGRVFR 524
DB      498 GHOSLTSGMELKDNILVSGNADSTVKIWDIKTG-----QCLQTLQGPKNQSAVTC 548
QY      525 LQFDEFQIVSSSHDDTILIWD 545
DB      549 LQFNKNFVITSSDDGTVKLD 569

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Search completed: April 25, 2005, 16:30:31
Job time : 136 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 25, 2005, 16:18:52 ; Search time: 42 Seconds

(without alignments)
1303.508 Million cell updates/sec

Title: US-09-415-795-4

Perfect score: 3034

Sequence: 1 MDPAAVAVQEKALKKFMNSE.....PAAQAEPSPSPRTTYISR 569

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2597	85.6	518	2	B48088
2	1635.5	53.9	701	2	T16607
3	690	22.7	506	2	T50211
4	590.5	19.5	605	2	T38932
5	545	18.0	640	2	S49932
6	531.5	17.5	650	2	T46660
7	520	17.1	579	2	T22703
8	519.5	17.1	267	2	S62507
9	455.5	15.0	1356	2	T18521
10	453	14.9	775	2	T45136
11	413.5	13.6	1227	2	AB1810
12	399	13.2	779	2	S56245
13	396.5	13.1	703	2	T43557
14	378.5	12.5	1189	2	AI2493
15	375	12.4	1747	2	AC1842
16	374	12.3	1526	2	AC2239
17	373.5	12.3	1258	2	AI2155
18	373.5	12.3	1683	2	AF2071
19	361.5	11.9	677	2	AB1861
20	358.5	11.8	559	2	AB2202
21	354	11.7	409	2	S36113
22	354	11.7	410	2	S48052
23	341	11.2	515	2	S19487
24	339.5	11.2	777	2	T41075
25	337	11.1	1146	2	A55532
26	336	11.1	676	2	AB2195
27	334	11.0	589	2	AG2400
28	333.5	11.0	1711	2	AD1842
29	332.5	11.0	317	2	T46032

30	330	10.9	333	2	G85034	probable WD-repeat
31	320	10.5	934	2	AG1889	WD-40 repeat prote
32	318	10.5	422	2	A56640	CDG4 repeat unit-c
33	313.5	10.3	376	2	T19266	hypothetical prote
34	312.5	10.3	714	2	S56893	hypothetical prote
35	312	10.3	786	2	AG2375	WD-40 repeat-prote
36	312	10.3	876	2	T51507	WD40-repeat protei
37	307.5	10.1	1693	2	S76066	beta transducin-1i
38	306.5	10.1	598	2	AE2415	WD-repeat protein
39	306	10.1	1189	2	AD2154	WD-repeat protein
40	305	10.1	704	2	S33263	transcription init
41	299.5	9.9	1194	2	T03818	apoptotic proteina
42	298	9.8	265	2	AF1890	WD-repeat protein
43	297.5	9.8	357	2	AI2099	WD-40 repeat prote
44	297	9.8	502	2	T41148	trp-asn repeat con
45	296.5	9.8	504	2	AG1837	WD-40 repeat prote

ALIGNMENTS

RESULT 1

B48088 beta-transducin repeat-containing protein - African clawed frog

N:Alternate names: beta-Trcp

C:Species: Xenopus laevis (African clawed frog)

C>Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 16-Aug-2004

C/Accession: B48088

R:Spevak, W.; Keiper, B.D.; Stratowa, C.; Caetanion, M.J.

Mol. Cell. Biol. 13, 4953-4966, 1993

A:Title: Saccharomyces cerevisiae cdc15 mutants arrested at a late stage in anaphase are

A:Reference number: A48088; MUID:93330289; PMID:8393141

A/Accession: B48088

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-518 <SPE>

A/Cross-references: UNIPROT:091854; GB:M98268; NID:G295542; PIDN:AAA02810.1; PID:G295543

C:Superfamily: WD repeat homology

C/Keywords: duplication

F:431-462/Domain: WD repeat homology <WD1>

Query Match 85.6%; Score 2597; DB 2; Length 518;

Best Local Similarity 91.6%; Pred. No. 5e-192;

Matches 488; Conservative 7; Mismatches 8; Indels 30; Gaps 1;

QY	18	SSEREDCNGGPPPKIPEKNSLRQTYNSCARLCINQETVCLASTAMTKENCVAATKLAN	77
DB	13	ASEREDCNRDEPPPKIPEKNTLRQ-----TKLAN	42
QY	78	GTSSMTIVKQKRLASVKEKEICVYKFEQMSSENOVEFVEHLISOMGHYGHINSYIK	137
DB	43	GTSSMTIVKQKRLASVKEKEICVYKFEQMSSENOVEFVEHLISOMGHYGHINSYIK	102
QY	138	PMLQRFITLALPARGLDIAENIISYLDKSLCAELVCKEYRYTSQGLMKLIERBV	197
DB	103	PMLQRFITLALPARGLDIAENIISYLDKSLCAELVCKEYRYTSQGLMKLIERBV	162
QY	198	RTDSLIRGLAERMGQYLFXNKKPPDGNAPPNSFYRALYPKIIDIETIESNMRGGRSL	257
DB	163	RTDSLIRGLAERMGQYLFXNKKPPDGNAPPNSFYRALYPKIIDIETIESNMRGGRSL	222
QY	258	ORIHRSFSTSGVYCLQYDDQKIVSGLRDNTIKIMDKNTLECKRLTGHGTSVLCLOYDE	317
DB	223	ORIHRSFSTSGVYCLQYDDQKIVSGLRDNTIKIMDKNTLECKRLTGHGTSVLCLOYDE	282
QY	318	RVIIITGSSDSITVRVWDVTGEMTLNLIIHCEAVLHLRPNNGMMVYCSKDRSIAVDMASP	377
DB	283	RVIIITGSSDSITVRVWDVTGEMTLNLIIHCEAVLHLRPNNGMMVYCSKDRSIAVDMASP	342
QY	378	TDITLRLVVGHRAAVNVVDQDKIVSAGDRITKWNVTSCGEVRLTLNGHKGIAICQ	437
DB	343	TDITLRLVVGHRAAVNVVDQDKIVSAGDRITKWNVTSCGEVRLTLNGHKGIAICQ	402

Qy	433	YRRLVVGSSDNTILAMP	IECGACLRVLEGHEELVRCIPGNRIYGAADGKITKMDL	497
Db	403	YRRLVVGSSDNTILAMP	IECGACLRVLEGHEELVRCIPGNRIYGAADGKITKMDL	462
Qy	498	VALDPRAPAGTICLT	LVHSGRVPRLOPDEFQVSSSHDTILAMP	550
Db	463	VALDPRAPAGTICLT	LVHSGRVPRLOPDEFQVSSSHDTILAMP	515

RESULT 2

Hypothetical protein K10B2.1 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
 C:Accession: J16607
 R:Miller, N.
 A:Submitted to the EMBL Data Library, June 1995
 A:Description: The sequence of C. elegans cosmid K10B2.
 A:Reference number: Z18545
 A:Accession: J16607
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-701 <MIL>
 A:Cross-references: EMBL:U28730, NID:9860694, PTD:9860695, PIDN:AAA68258.1, CESP:K10B2.1
 A:Experimental source: Strain Bristol N2
 C:Genetics:
 A:Gene: CESP:K10B2.1
 A:Introns: 78/3; 125/1; 183/2; 281/3; 404/3; 551/3; 668/3
 Query Match 53.9%, Score 1635.5, DB 2, Length 701;
 Best Local Similarity 57.7%, Pred. NO. 8.2e-118;
 Matches 328; Conservative 69; Mismatches 116; Indels 55; Gaps 8;

```

Query March 53.9#: Score 1635.5; DB 2; Length 701;
Best Local Similarity 57.7#: Pred. No. 8.2e-118;
Matches 328; Conservative 69; Mismatches 116; Indels 55; Gaps 8;

QY 31 RKIIPEKNSLRLQTYNSCARLCLNQETVCLASTAMKTENCYAKTKLAN-----GTS 80
D 2 RRFEGKRALTKQGRARDGSGSIQALTVCSV-----IERCF--TAVSNIFFLSTFSEVF 55
QY 81 SMIVPKQR-----KLASYEKEKELCVYTFQWSESQDVEVEVHLISGMCHYQGHINSY 135
D 56 SFLPSPRTQIFLSYSRSFSSFFSEVL-----KMBEHEDLPMDKIVHLSHYLGKQDNF 110
QY 136 LKPMLODFITALPARGLDHIAENILSYLDAKSLCAAEIYCKEWYRVYSDGMLWKLIER 195
D 111 IRPMLQRFINLPR-----HLVELILFNVNSDLKSCFVSTSRCALARGCHMKKILIEK 166
QY 196 MWTDSLWRLGIAERGGWGYL-----FKCKPDPGAPNSFYRAL 235
D 167 NVRSDSLWGGISEKQWMDKFLNISRDMSVRRICEKFNVDVNIKKDKLDQLILMHVFYSKL 226
QY 236 YPKIIIDLETIESMWRGCRHSIORIHCRSEFSKGYVCLQYQDOKIVSGLRDNTIKIMQKN 295
D 227 YPKIIRIDHINIDNNKRGNYKQTRINCOSENSKGYVCLQYQDOKIVSGLRDNTIKIMQKN 286
QY 296 TLECKRILTGHGTSVLCLOYDERVLIITGSSDSTVRVMDVNTGEMLNTLIHHCEAVLHLRF 355
D 287 DYSCSRILSGHTGSLCLQYDNRVLISSGSATYRVMDVEVEGECKITLIHHCEAVLHLRF 346
QY 356 NNGMMVYTSKSRSLAVWMDMASPTDITLRLVYGRHAANVYDFDDKYIVSASGDRITIKW 415
D 347 ANGIMVYTSKSRSLAVWMDVSPRDIITIRVLYVGHAAVNVDFDRIYVVSASGDRITIKW 406
QY 416 NTSTCEPRTLNGHGRGIACLOYRDLVVGSSSDPTITLMDIEGACCLRVYEGHEBELVRC 475
D 407 SMDTLEFPRTLAGHRGIIACLOYRGLVVGSSSDNTITLMDIHSVCRLVYEGHEBELVRC 466
QY 476 IRFDNKRIVSGAYDGIKIVMDLVAALDPRAPAGTICLTLLVEHSGRVERLQFDEFQIVSS 535
D 467 IRPDEKRIVSGAYDGIKIVMDLQALDPRALSEICLSLVQHTGRVFRLOFDPQIVSS 526
QY 536 SHDDTILWDFLNDPAPAAQEPSPRSRT 563
D 527 SHDDTILWDFLNDAP-----PSGLPSSST 549

```

RESULT 3

MD-repeat protein [imported] - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #ext_change 16-Aug-2004
C:Accession: T50211
R:McDonagall, R.C.; Rajandream, M.A.; Barrell, B.G.; Brown, S.; Murphy, L.; Jones, L.; McI
submitted to the EMBL Data Library, January 2000
;Reference number: Z25046

A; Molecu

A;Cross-references: UNIPROT:Q09885; EMBL:AL136538; PDB:CB66464.1; GSPDB:GND00066; SPDB:
A;Experimental source: strain 972h(-); cosmid C30
C;Genetics:
A;Gene: SPAC29E6.01; SPDB:SPAC30.05
A;Map position: 1
A;Intons: 43/1; 74/3
C;Superfamily: WD repeat homology

Query Match	22.7%;	Score 690;	DB 2;	Length 506;
Best Local Similarity	30.4%;	Pred. No. 3,3e-45;		
Matches 163; Conservative 104; Mismatches 167; Indels 102; Gaps 15;				

[illegible]

RESULT 4

probable sulfur metabolite control protein - fission yeast (*Schizosaccharomyces pombe*)
C;Species: *Schizosaccharomyces pombe*
C;Date: 03-Dec-1999 #sequence_rev: 03-Dec-1999 #ext_change: 16-Aug-2004
C;Accession: T38932
R;Badcock, K.; Churcher, C.M.; Wood, V.; Barrell, B.G.; Randle, M.A.
submitted to the EMBL Data Library, April 1997
A;Reference number: Z21818
A;Accession: T38932

A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-605 <BAD>
 A:Cross-references: UNIPROT:P87053; EMBL:Z94864; PIDN:CAB08168.1; GSPDB:GN00066; SPDB:SF
 A:Experimental source: strain 972h-, cosmid c57A10
 C:Genetics:
 A:Gene: SPDB:SPAC57A10.05c
 A:Map position: 1
 C:Superfamily: WD repeat homology

Query Match: 19.5%; Score 590.5; DB 2; Length 605;
 Best Local Similarity 29.0%; Pred. No. 1.9e-37;
 Matches 156; Conservative 86; Mismatches 189; Indels 107; Gaps 12;

QY 80 SSMIVPKOKKLSASIEKEKELCVKFEQMSF---SDQVEFVHLISOMCHYGHINSL 136
 DB 46 SSM---HNEISGLSEKSRQRYEAWAFAFEASCERKALQGIINSSSLSPASSTL 101
 QY 137 KPMLODFPTALPARGLDHIENILSYLDAKSLCAAEIVCKEYRVTSQMLMKLIERM 196
 DB 102 DSLVLDLPLSLPV---EISFRILSPIDARSLQQAQVSKMKELADDDVIMHMCQH 157
 QY 197 VRTDLSLWGLAEERRGQVLFKN----- 219
 DB 158 INRK-----CEKCGMGLPLERNTLYAKASIQRYERLTKRGVDQAHESSPVAKKLD 211
 QY 220 -----KPPDGNAPPSNF-----YALPKIIOIETTESMWRGCRHSLQ 258
 DB 212 DYPSSNEETISSVPRPSPNSKFEFLPKTRPMREYVAERCR---VECMRHR----- 263
 QY 259 RIHCR-----SETSKVYCLQYDDQKIVSGLRNTIKIMDKTLECKRIITGHTSVLCQ 314
 DB 264 ---CQOVLVSGHSDVCLQVRLNITLASSYDATTILMLMTLTFQVALLEGHSSVTLQ 320
 QY 315 YDERVIITGSSDSTVRVDVNTGEMLNTLIHCEAVLHLRFNNGMVTCSKDRSIAVDM 374
 DB 321 FDQCLTIGSMDKIRINMYRTSECSILHGHSTSVLCITFPTSLVSGSADCTVKLMHF 380
 QY 375 ASPDITLRVLVGRRAVNVDF--DDKIYVSAAGDRTIKVWNTSTGEFVTLNGHKG 432
 DB 381 SGGKRITLR---GHTGPNVSVRIIRDRGLVYSGSDSTIKIWSLETYVCLHTFSAHGP 436
 QY 433 IACIQYRDLVYSSGSDNTIRLMDIEGACLVLSGHELVLCIFDNKRIYVSGADKI 492
 DB 437 VQSLADSLRPLSCGLDGTIKOMDIEKKCVHTLFGHIEGWELIADHRLISGADGV 496
 QY 493 KVMDLVAALDPRAPAGTLCRLTVLHSGRVFRLQFDEFOIVSSSHDDTLLIWDPLNDP 550
 DB 497 KVMACE-----CVHTLKNHSEPVTSVALGDCEVVGSGEDKITYLMLFNNAP 543

RESULT 5

MET30 protein - yeast (*Saccharomyces cerevisiae*)
 S49932
 N:Alternate names: protein Y1905.02; protein Y1L046w
 C:Species: *Saccharomyces cerevisiae*
 C>Date: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 16-Aug-2004
 C:Accession: S49932; S43750
 R:Odell, C.; Bowman, S.
 submitted to the EMBL Data Library, December 1994
 A:Reference number: S49931
 A:Accession: S49932
 A:Molecule type: DNA
 A:Residues: 1-640 <ODS>
 A:Cross-references: UNIPROT:P39014; GB:Z47047; EMBL:Z46861; NID:g603997; PID:g763300; MI
 R:Thomas, D.; Cherest, H.; Barbey, R.; Sudin-Kerjan, Y.
 submitted to the EMBL Data Library, December 1993
 A:Reference number: S43750
 A:Accession: S43750
 A:Molecule type: DNA
 A:Residues: 1-60, 'I', 62-640 <THO>
 A:Cross-references: EMBL:L26505; NID:g432493; PID:g432494
 C:Genetics:

A:Gene: SGD:MET30
 A:Cross-references: SGD:S0001308; MIPS:Y1L046w
 A:Map position: 9L
 C:Superfamily: WD repeat homology
 F:298-329/Domain: WD repeat homology <WD1>
 F:338-369/Domain: WD repeat homology <WD2>
 F:374-409/Domain: WD repeat homology <WD3>
 F:417-450/Domain: WD repeat homology <WD4>

Query Match: 18.0%; Score 545; DB 2; Length 640;
 Best Local Similarity 28.9%; Pred. No. 6.6e-34;
 Matches 167; Conservative 85; Mismatches 202; Indels 124; Gaps 17;

QY 34 IPEKSLQGTNSCARLCLN-QETVCLASTAMKENCVAK-TKLANGSSMIVPKOKKLS 91
 DB 86 LPEVNFYFCYRHNPDIDFSPHTACYKODLKRTOEINANIAKPLQEQSDIHIIISKYS 145
 QY 92 ASYEKEKELCVKFEQMSFQVEFVHLISOMCHYGHINSLYKPMLODFPTALPAR 151
 DB 146 NSNDKIRL-----ILDGILSTSCFPQSLYSISLVTHMKIDFISILP-- 188
 QY 152 GLDHIENILSYLDAKSLCAAEIVCKEYRVTSQMLMKLIERMVRTDSLWGLAERR- 210
 DB 189 --QELSLKILSYLDCQSLCNATRVCRKQKXLADDDRVVYHMCQH-----DRKC 236
 QY 211 ---GMQVLFYFNK-----PPDGNAPPSNFYALPKIIOIETTESMWRGCRHSLQ 258
 DB 237 PNCGMGLPLHMKRARLQONSTGSSSNADIQTTTRPKVIVIRERFVESNRKG----- 291
 QY 259 RIHCRSEFSK---GVYCLQYDDQKIVSGLRNTIKIMDKTLECKRIITGHTSVLCQ 314
 DB 292 --HCRIOEFKHMGVLLQFNRYLLFTGYSVSTIGVWDTGKLIIRLSGHSDDVTKLY 349
 QY 315 YDERVIITGSSDSTVRVDVNTGEMLNTLIHCEAVLHLRFNNGMVTCSKDRSIAVDM 374
 DB 350 FDDRKLITGSLDKTIRVWNYITGECISTYRGHSVLSVDSYOKIYVSGADKTVKMHV 409
 QY 375 ASPDITLRVLVGRRAVNVDFPDKI--VSASGDRTIKVWNTSTGEFVTLNGH--- 429
 DB 410 ESRCTYTLR---GHTGVNVCVKLHPKSPSCPSGDDTTIRMDIRITNSCLKVFRGHVQ 465
 QY 430 KRGIAQLQYRD--RLVSGSS----- 448
 DB 466 VQKIIPLTIKVENLATDNTSDSSPODDPTMTGACADSDTPSNQETVLDENITPYPHL 525
 QY 449 ---DNTIRLMDIEGACLVLSGHELVLCIFDNKRIYVSGAYDKIKYMDLVAALDP 503
 DB 526 LSCGLDNTIKIMDVYTGKCIPTQFGHVGWMDIADNFRITISGSHDSIKYMDLQSG--- 582
 QY 504 RAPAGTLCRLTVLHSGRVFRLQFDEFOIVSSSHDDTI 541
 DB 583 ---KCMHTF---NGR--RLQRETOHTOTQSLGDKV 609

RESULT 6

T46660
 sulfur controller-2 protein [imported] - *Neurospora crassa*
 C:Species: *Neurospora crassa*
 C>Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 16-Aug-2004
 C:Accession: T46660
 R:Kumar, A.; Paletta, J.V.
 Proc. Natl. Acad. Sci. U.S.A. 92, 3343-3347, 1995
 A:Title: The sulfur controller-2 negative regulatory gene of *Neurospora crassa* encodes a
 A:Reference number: T23121; MUID:95241499; PMID:7724564
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-650 <KUM>
 A:Cross-references: UNIPROT:O01277; EMBL:U17251; NID:g806757; PIDN:AAA68968.1; PID:g8067
 C:Genetics:
 A:Gene: scon-2
 A:Map position: 3
 A:Introns: 75/3; 319/1; 354/1

Matches 150; Conservative 78; Mismatches 222; Indels 70; Gaps 17.

Db 120 TGLIVTASSDRTLRTWDITTGHCIRIHAHQRGIAQAQYNGKFVSGSSDLTIRIFEASS 175

Db 589 SMDTIRIWDLENIMWNGECYSATNSASPCAKILGMATYLQGHETALVELLRISDKRYLSA 648
 QY 536 SHDDTILITWDFLNDPAQAQEPSPSPRTTTY 566
 Db 649 AADGSIRGWD-AND-----YSRKFST 668

RESULT 13

T43557
 F-box/WD-repeat protein pop2 - fission yeast (Schizosaccharomyces pombe)
 N/Alternate names: proteolysis factor sud1p
 C/Species: Schizosaccharomyces pombe
 C/Date: 21-Jan-2000 #sequence revision 21-Jan-2000 #text_change 09-Jul-2004
 C/Accession: T43557; T38794; T43798
 R/WOLF, D.A.; Jackson, P.K.

submitted to the EMBL Data Library, December 1997
 A/Description: Fission yeast pop2 encodes a novel F-box/WD-repeat protein involved in cell cycle regulation
 A/Reference number: Z22576
 A/Accession: T43557

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-703 <MW>

A/Cross-references: UNIPROT:O14170; EMBL:AF038867; PIDN:AAB95480.1

A/Experimental source: strain h-972

R/Gentles, S.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.

submitted to the EMBL Data Library, August 1996

A/Reference number: Z21812

A/Accession: T38794

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-703 <GEN>

A/Cross-references: EMBL:Z98602; PIDN:CA31275.1; GSPDB:GN00066; SPDB:SPAC4D7.03

A/Experimental source: strain 972h; cosmid c4D7

R/Jallepalli, P.V.; Tien, D.; Kelly, T.J.

Proc. Natl. Acad. Sci. U.S.A. 95, 8159-8164, 1998

A/Title: Sud1+ targets cyclin-dependent kinase-1-related Cdc18 and Rrm1 proteins for ubiquitination

A/Reference number: Z22686; MUID:98318628; PMID:9653157

A/Accession: T43798

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-703 <JAL>

A/Cross-references: EMBL:AF064515; NID:g3293382; PIDN:AAC39496.1; PID:g3293383

C/Genetics:

A/Gene: pop2; sud1; SPAC4D7.03

A/Map position: 1

C/Function:

A/Description: required to prevent spontaneous re-replication

Query Match 13.1%; Score 396.5; DB 2; Length 703;
 Best Local Similarity 23.3%; Pred. No. 26-22;
 Matches 146; Conservative 92; Mismatches 226; Indels 163; Gaps 25;
 QY 14 KFNSSERED-CNNGEPPRKI-----IPEKSLQTYNSCARCLT---NQETVCL 59
 Db 96 KFNSEIENVSYCLDHSPPDSVPDPFSISLVQKRF--YSHSLSPKIIISIDRRNRKID 154
 QY 60 ASTAMKTECAKYKLANGTSMIVPKOKLSASTEK-EKEICVYFEQWSESDOVEFE 118
 Db 155 NSISNSNFPSPKPV--DTSMTVSPGSKPISSEDELDNLQSIQTFEDLPBGIO-SYAF 211
 QY 119 HLISQMGYHGH-INSYLKPMLODFITLAPARGDHAENIISYLAKSICAEALYCK 177
 Db 212 FOLMSCKRQSRMLLNECEPLKDOIISNLPF---STVOSILNLDHSLSCRLVSP 267
 QY 178 EMYRV---TSDGMLMKKLIEMRVRTDSLMGLAERRGQYLFRNKPDPDGNAP---N 229
 Db 268 TWRNRLDVHTS--YMKMF-----SLFGQINENMW---KYAPNMLNRPFLIND 312
 QY 230 SFYRLAYPKLIIDITETISNMFGRHSIOR----- 259
 Db 313 QISDDYFPEIFK-----RHFLNRKRWLPSPISIPSHLSPIHVNFMITSLHL 360

QY 260 -----IHCRSETSK-GVYCLQDDPKIVSGLRNTIKIWDKNT 296
 Db 361 KDRITTSGGSGTIOIHNAITGLVLEARLKGKAGVAWKHENTLVSGSIDKTVRWNIK 420
 QY 297 IECKRIILGHTGSLVLCQY-----DERVIITGSSDSIVRVWDVNTGEM 340
 Db 421 AKCTHIFRHSIIRICLEILVPSRLIRHVEIVEPDPQYIVSGSRDHLRV----- 472
 QY 341 NTLHHCEAVLHRRNMGMTCSKDRSIAWDMASPDIDITLRLVGHRAVNVVDFD 400
 Db 473 -----KLPRNTPPYLPDNTNSIDRWE-KNPFV--HTLIGHITDSVKTISGXG 517
 QY 401 KYIVASGDRITKVNNTSCFEVFTLNGHKGRIACLOYRD--RLVVGSSDNTIRLMD 458
 Db 518 DILVSGSDSSIRIRVVTGECTYLHGRHSRLRYSVLYEPENITCISGMSDSIRVMD 577
 QY 459 CGACRLVLEGHELVRCIRPDKRIVSGAYDGIKIVMDLVVALDPRAPAGTLCLRTLYEH 518
 Db 578 TGTCKYVLEGHDAFYTLLNVPQNRLISGSADSTIRIWD---LNTGKP-----LMVLP 628
 QY 519 SGVRFLQDFEQIVSSSHDITLIWD 545
 Db 629 SGYISSFVSDERKTI-SGNDGSVKLMD 654

RESULT 14

WD-repeat protein [imported] - Nostoc sp. (strain PCC 7120) plasmid PCC7120alpha
 A/Species: Nostoc sp. PCC 7120
 A/Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C/Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

C/Accession: A12493

R/Kaneko, T.; Nakamura, Y.; Molk, C.P.; Kuritz, T.; Saeemoto, S.; Watanabe, A.; Iritiguchi

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.

DNA Res. 8, 205-213, 2001

A/Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena

A/Reference number: A11807; MUID:21595285; PMID:11759840

A/Accession: A12493

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-1189 <KUR>

A/Cross-references: UNIPROT:O8VLO9; GB:BA000020; PIDN:BAW78213.1; PID:g17135667; GSPDB:G

C/Genetics:

A/Gene: alr7129

A/Genome: plasmid

Query Match 12.5%; Score 378.5; DB 2; Length 1189;
 Best Local Similarity 26.7%; Pred. No. 1e-20;
 Matches 96; Conservative 63; Mismatches 107; Indels 93; Gaps 10;
 QY 280 IVSGLRNTIKIWDKNTLECKRIILGHTGSLVLCLOYD--ERVITGSSDSIVRVWDVNTG 337
 Db 745 LASGSFDQNVMLADHTGKCVMTLQHGTVTSVAFNPKMULLSGSYDSQVKVMDRKTG 804
 QY 338 EMLNLTLLHHCNAVHLARN----- 356
 Db 805 RCLDTLKGHTNRINSVAFHPQGLFVSGDDHAAKIMELGTGQCIKTGQHSNATYTTAH 864
 QY 357 ---NGMWVTSKDRSIAWDMASPDIDITLRLVGHRAVNVVDFD--KYIVS 405
 Db 865 NWEHSLASGHEDQITKIMDLNHSFHSNNTVHFRILQGHSNRVSFVSSTGQLLAS 924
 QY 406 ASGDRITKVNNTSCFEVFTLNGHKGRIACLOYR--DLVVGSSDNTIRLMDIEGAC 463
 Db 925 GSADRTITLMSPHGTQCLHTLHGSGVWMAIAFSDDKLASGYDHTVKIMDVSSGCL 984
 QY 464 RVLGHEHLYVRCIRPDKRIVSGAYDGIKIVMDLVVALDPRAPAGTLCLRTLYEH 518
 Db 985 QTLQHPGSVALAVASCDGKTLFSSGYHKLVKQMDVETGYCLQTEWADSNRVMAVAVRD 1044
 QY 504 RAPAGT-----LCRLTVEHSGRVFRLQF--DEFQIVSSSHDDITLIWD 545

Db 1045 NQYLATGGDDSVRLWDIGKVCVRTFSGHTSQVICILETKDGRMISSSSDRTIKIWN 1103

RESULT 15

AC1842

WD-40 repeat protein [imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp. PCC 7120

A/Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C;Date: 14-Dec-2001 #sequence 14-Dec-2001 #text_change 09-Jul-2004

C;Accession: AC1842

R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,

Nakazaki, N.; Shimpō, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.

DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena

A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AC1842

A;Status: preliminary

A; molecule type: DNA

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A;Residues: 1-1747 <KUR>
```

A/Cross-references: UNIPROT:Q8Z020; GB:BA000019; PIDN:BAE77807.1; PID:q17135261; GSPDB:Q

A: Experimental source: strain PCC 7120

C:Genetics:

A:Gene: [a110283](#)

Query Match 12.48; Score 375; DB 2; Length 1747;

Best Local Similarity 32.78; Pred. No. 3.3e-20;

Matches 84; Conservative 50; Mismatches 107; Indels 16; Gaps 7;

QY 276 DDQKIVSGLRDNTIKIMDKNTLECKRILTGHTGSVLCLQ--DERVIITGSSDSTVRVMD 333

[illegible]

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QY 334 VNTGEMLNTLIHCEAVLHLRF--NNGMMVTCSKDRSIAVMDMASPTDITLRRVLVGHRA 391

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Db      1547 VNDGOLLRLTGHNDEVTSVNFSFDPGOFILASGSTDNTVKIWO-----TDGRLKNITGHGL 1600

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Db 1603 AIASVKFSPDSHTLASASWDNTIKLWOVTDGKLINNLNGHIDGVTSLSFSPDGEILASGS 16622

QY 448 SDNTIRLWDIEGACLRVLEGHEELVRCIRF--DNKRIVSGAYDGKIKWMDLVAALDPRA 505

21

[illegible]

OV 506 PAGTICLRTLVESGRV 522

Dd 1721 00GCDRTDYLQHSNV 1737

DD I /Z I QGCDRI IDIEUHSNV I /S I

Search completed: April 25, 2005, 16:31:20
Job time : 45 secs

Job time : 45 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 25, 2005, 16:27:33 ; Search time 179 Seconds

(without alignments)
1627.782 Million cell updates/sec

Title: US-09-415-795-4

Perfect score: 3034
Sequence: 1 MDPAAVLIQEKALKFMNSSE.....PAAQAEPSPSPRTYITISR 569

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: uniprot_sp|prot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3006	99.1	605	1 FMA1 HUMAN	Q9Y297 homo sapien
2	2997	98.8	569	2 Q9QU15	Q9QU15 mus musculu
3	2990	98.5	569	2 Q9G159	Q9G159 mus musculu
4	2978	98.2	569	2 Q9R1G7	Q9R1G7 mus musculu
5	2821	93.0	564	2 Q68DS0	Q68DS0 mus musculu
6	2597	85.6	518	1 TRCB XENLA	Q91854 xenopus lae
7	2395	78.9	529	2 Q8BY90	Q8BY90 mus musculu
8	2384.5	78.6	542	1 FMA1 HUMAN	Q9UKD1 homo sapien
9	2380	78.4	563	2 Q8KO22	Q8KO22 mus musculu
10	2360	77.8	555	2 Q8CHD5	Q8CHD5 mus musculu
11	2286	75.3	563	2 Q923H0	Q923H0 mus musculu
12	2258.5	74.4	527	2 Q6PGM4	Q6PGM4 brachydanto
13	2250	74.2	527	2 Q7ZVZ1	Q7ZVZ1 brachydanto
14	2128	70.1	621	2 Q86SD3	Q86SD3 ciona intes
15	2089.5	68.9	510	2 Q4382	Q4382 ciona intes
16	2089.5	68.9	510	2 Q9VDE3	Q9VDE3 dirosophila
17	1948.5	64.2	555	2 Q7PYH7	Q7PYH7 anopheles g
18	1638.5	54.0	665	1 LI23 CAEEL	Q09990 caenorhabdi
19	1498	49.4	430	2 Q9BJS4	Q9BJS4 heterodera
20	1230	40.5	252	2 Q922C7	Q922C7 mus musculu
21	690	22.7	506	1 PORB SCHPO	Q09855 schizosacch
22	675.5	22.3	1083	2 Q7Q7E2	Q7Q7E2 anopheles g
23	661	21.8	1326	2 Q9VZP4	Q9VZP4 dirosophila
24	640	21.1	707	1 FBM7 HUMAN	Q969H0 homo sapien
25	639	21.1	629	1 FBM7 MOUSE	Q8UNV4 mus musculu
26	638	21.0	122	2 Q8UTN3	Q8UTN3 xenopus lae
27	621.5	20.5	755	2 Q7S199	Q7S199 neurospora
28	618.5	20.4	520	2 Q6COT5	Q6COT5 yarrowia li
29	590.5	19.5	605	2 POR1 SCHPO	Q87053 schizosacch
30	583	19.2	1010	2 Q7RMG8	Q7RMG8 neurospora
31	575	19.0	678	1 SCOB_EMENT	Q00659 emericella

32	556	18.3	569	2 Q7SAK9	Q7SAK9 ashyba goss
33	545.5	18.0	623	2 Q6C1D5	Q6C1D5 kluyveromyc
34	545	18.0	640	1 MTJ0 YEAST	P39014 saccharomyc
35	541.5	17.8	667	2 Q6BRQ3	Q6BRQ3 debaryomyce
36	539.5	17.8	741	2 Q6EM92	Q6EM92 debaryomyce
37	531.5	17.5	650	1 SC02 NEUCR	Q01277 neurospora
38	527	17.4	673	2 Q6FLT6	Q6FLT6 candida gla
39	520	17.1	587	1 SE10 CAEEL	Q93794 caenorhabdi
40	514	16.9	581	2 Q6CH88	Q6CH88 yarrowia li
41	503	16.6	1029	2 Q7S2D9	Q7S2D9 neurospora
42	489.5	16.1	650	2 Q7RYJ1	Q7RYJ1 neurospora
43	477.5	15.7	684	1 CDC4 CANAL	P53699 candida alb
44	469	15.5	1376	2 Q8X1P2	Q8X1P2 podospora a
45	468.5	15.4	698	2 Q6C5T6	Q6C5T6 yarrowia li

ALIGNMENTS

RESULT 1	FWA1 HUMAN	STANDARD;	PRT;	605 AA.
AC	Q9Y297; Q9Y213;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	F-box/WD-repeat protein 1A (F-box and WD-repeats protein beta-TrCP)			
DE	(E3RSIKappab) (pikappabalpha-E3 receptor subunit).			
GN	Name=BTRCP; Synonyms=BTRCP, FBW1A, FBXW1A;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RX	MEDLINE=99075339; PubMed=9859996; DOI=10.1038/25159;			
RA	Varon A., Hatrubal A., Davis M., Lavon I., Amit S., Manning A.M.,			
RT	Andersen U.S., Mann M., Mercurio F., Ben-Neriah Y.,			
RT	"Identification of the receptor component of the IkappaBalpha-			
RT	ubiquitin ligase.";			
RL	Nature 396:590-594 (1998).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM 2).			
RC	TISUE=Lymphoid;			
RX	MEDLINE=98325370; PubMed=9660940; DOI=10.1016/S1097-2765(00)80056-8;			
RA	Margottin F., Bour S.P., Durand H., Selig L., Benichou S., Richard V.,			
RA	Thomas D., Strebel K., Benarous R.;			
RT	"A novel human WD protein, h-beta-TrCP, that interacts with HIV-1 Vpu			
RT	connects CD4 to the ER degradation pathway through an F-box motif.";			
RL	Mol. Cell 1:565-574 (1998).			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM 2).			
RX	MEDLINE=20003060; PubMed=10531035; DOI=10.1016/S0960-9822(00)80020-2;			
RA	Cenziarelli C., Chiau D.S., Guardavaccaro D., Parks W., Vidal M.,			
RA	Pagano M.;			
RT	"Identification of a family of human F-box proteins.";			
RL	Curr. Biol. 9:1177-1179 (1999).			
RN	[4]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISUE=Brain;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Schenker C.M., Schuler G.D.,			
RA	Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinci P., Prange C.,			
RA	Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bosch S.A., McEwan P.J., McKernan K.C., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,			

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.L., Skalska U., Smalins D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[5]
RN CHARACTERIZATION.
RP MEDLINE=99145464; PubMed=9990852;
RX Winston J.T., Strack P., Beer-Romero P., Chu C.Y., Ellledge S.J.,
RA Harper J.W.;
RT "The SCF(beta-TRCP)-ubiquitin ligase complex associates specifically
RT with phosphorylated destruction motifs in I-kappa-B-alpha and beta-
RT catenin and stimulates I-kappa-B-alpha ubiquitination in vitro.";
RL Genes Dev. 13:270-283 (1999).
[6]
RN INTERACTION WITH UBQLN1.
RP TISSUE=B-cell;
RX MEDLINE=20437281; PubMed=10983987; DOI=10.1016/S1097-2765(00)00040-X;
RA Kleijnen M.F., Shih A.H., Zhou P., Kumar S., Soccio R.E.,
RA Keldersma N.L., Gill G., Howley P.M.;
RT "The hPLIC proteins may provide a link between the ubiquitination
RT machinery and the proteasome.";
RL Mol. Cell 6:409-419 (2000).
[7]
RN INTERACTION WITH PHOSPHORYLATED CTNNB1.
RP MEDLINE=22072105; PubMed=12077367;
RX Sadot E., Conacci-Sorrenti M., Zhurinsky J., Shnitzer D., Lando Z.,
RA Zharhary D., Kam Z., Ben-Ze'ev A., Geiger B.;
RT "Regulation of S33/S37 phosphorylated beta-catenin in normal and
RT transformed cells.";
RL J. Cell Sci. 115:2771-2780 (2002).
[8]
RN X-RAY CRYSTALLOGRAPHY (2.95 ANGSTROMS) OF 175-605 IN COMPLEX WITH SKP1
RP AND CTNNB1.
RX MEDLINE=22706071; PubMed=12820959; DOI=10.1016/S1097-2765(03)00234-X;
RA Wu G., Xu G., Schulman B.A., Jeffrey P.D., Harper J.W.,
RA Pavletich N.P.;
RT "Structure of a beta-TrCP1-Skp1-beta-catenin complex: destruction
RT motif binding and lysine specificity of the SCF(beta-TrCP1) ubiquitin
RT ligase.";
RL Mol. Cell 11:1445-1456 (2003).
[9]
RN FUNCTION: Substrate-recognition component of the SCF (SKP1-CUL1-F-
RP box protein) ubiquitin ligase complex, which mediates the
RX ubiquitination of proteins involved in cell cycle progression,
RA signal transduction and transcription. Regulates the stability of
RA CTNNB1 and participates in Wnt signaling.
CC CTNNB1 and participates in Wnt signaling.
CC -1- PATHWAY: Ubiquitin conjugation; third step.
CC -1- SUBUNIT: Interacts directly with SKP1 in the SCF complex.
CC Interacts specifically with phosphorylated CTNNB1 and NFKBIA,
CC ubiquitination substrates. Binds UBQLN1.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- ALTERNATIVE PRODUCTS:
CC Name=1;
CC Name=2;
CC IsoId=Q9Y297-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9Y297-2; Sequence=VSP_006764;
CC -1- SIMILARITY: Contains 1 F-box domain.
CC -1- SIMILARITY: Contains 7 WD repeats.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF101784; AAD08702.1; -.
CC EMBL; Y14153; CAA74572.1; -.

DR EMBL; AF129530; AAF04464.1; -.
DR EMBL; BC027994; AAB27994.1; -.
DR PDB; 1P22; X-ray; A=171-605.
DR Genew; HGNC:1144; BIRC.
DR MIM; 603482; -.
DR GO; GO:0004840; F:ubiquitin conjugating enzyme activity; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR GO; GO:0006511; P:ubiquitin-dependent protein catabolism; TAS.
DR InterPro; IPR001810; F-box.
DR InterPro; IPR008945; Skp1_Skp2.
DR InterPro; IPR001680; WD40.
DR InterPro; IPR011046; WD40_1like.
DR Pfam; PF00646; F-box; 1.
DR Pfam; PF00400; WD40; 7.
DR PRINTS; PR00320; GPROTEINRPT.
DR ProDom; PD000018; WD40; 4.
DR SMART; SM00256; FBOX; 1.
DR SMART; SM00320; WD40; 7.
DR PROSITE; PS50181; FBOX; 1.
DR PROSITE; PS00678; WD_REPEATS_1; 6.
DR PROSITE; PS50082; WD_REPEATS_2; 7.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
DR 3D-structure; Alternative splicing; Ligase; Repeat;
KW Ub1 conjugation pathway; WD repeat; Wnt signaling pathway.
FT DOMAIN 190 228
FT REPEAT 301 338 WD 1.
FT REPEAT 341 378 WD 2.
FT REPEAT 381 418 WD 3.
FT REPEAT 424 461 WD 4.
FT REPEAT 464 503 WD 5.
FT REPEAT 505 541 WD 6.
FT REPEAT 553 590 WD 7.
FT VARSPLIC 17 52
FT Missing (in isoform 2).
FT /FtId=VSP_006764.
FT HELIX 180 183
FT TURN 184 184
FT HELIX 185 187
FT TURN 188 188
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FT TURN 198 199
FT HELIX 202 211
FT HELIX 213 221
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FT TURN 286 288
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FT STRAND 458 463
FT STRAND 469 475

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FT      TURN      476      477
FT      STRAND    478      483

Query Match      99.1%; Score 3006; DB 1; Length 605;
Best Local Similarity 94.0%; Pred. No. 1.2e-217;
Matches 569; Conservative 0; Mismatches 0; Indels 36; Gaps 1;

QY      1  MDPAAVAVLOEKALKFM-----NSSSRREDC 24
DB      1  MDPAAVAVLOEKALKFMCSMPRSIMWAGCSSLWNTSMBSRLCLVNPFGALTAFOUSSREDC 60

QY      25  NNGEPPRKIIPEKNSLRQTYNSCARLCLNOETVCLASTAMKTENCVAKTLANGTSSMIV 84
DB      61  NNGEPPRKIIPEKNSLRQTYNSCARLCLNOETVCLASTAMKTENCVAKTLANGTSSMIV 120

QY      85  PRQRLKLSAYEKEKELCVKFEQWSESDOVEFEVHLISQMCHYOHGHINSYKPMLOQDF 144
DB      121  PRQRLKLSAYEKEKELCVKFEQWSESDOVEFEVHLISQMCHYOHGHINSYKPMLOQDF 180

QY      145  ITALPARGLDHIAENILSYLDAKSLCAAEVCKEWRVTSDDMLMKKLIERNVRTDSLMR 204
DB      181  ITALPARGLDHIAENILSYLDAKSLCAAEVCKEWRVTSDDMLMKKLIERNVRTDSLMR 240

QY      205  GLAERRGMGOYLFFKXKPPDGNAPNSFYALYPKIIODIETIESNWRGSHLORHCRS 264
DB      241  GLAERRGMGOYLFFKXKPPDGNAPNSFYALYPKIIODIETIESNWRGSHLORHCRS 300

QY      265  ETSKGVYCLQYDDOKIVSGLRDNTIKINDKNTLECKRIITGHTGSLVCLQYDERVITGS 324
DB      301  ETSKGVYCLQYDDOKIVSGLRDNTIKINDKNTLECKRIITGHTGSLVCLQYDERVITGS 360

QY      325  SSTSTRVMDVNTGEMLNTLIHCEAVLHIFRNNGMNVTSKCRSLAVMDMASPTDITLR 384
DB      361  SSTSTRVMDVNTGEMLNTLIHCEAVLHIFRNNGMNVTSKCRSLAVMDMASPTDITLR 420

QY      385  VLVGRRAAVNVDPDDKYIVSASGDRITIKVNTSTCEFEVTLNGHKRGACIQYDRILV 444
DB      421  VLVGRRAAVNVDPDDKYIVSASGDRITIKVNTSTCEFEVTLNGHKRGACIQYDRILV 480

QY      445  SSSSNTTRTLMIDIEGACLRVLEGHEBELVRCIRFPNKRIVSAGYQGIKVMPLVALDPR 504
DB      481  SSSSNTTRTLMIDIEGACLRVLEGHEBELVRCIRFPNKRIVSAGYQGIKVMPLVALDPR 540

QY      505  APAGTLCRTIYHSGRVRLQDFEFOYSSSHDPTLIMDLNPAQAEPSPSPRY 564
DB      541  APAGTLCRTIYHSGRVRLQDFEFOYSSSHDPTLIMDLNPAQAEPSPSPRY 600

QY      565  TYISR 569
DB      601  TYISR 605

RESULT 2
Q90U15  PRELIMINARY; PRT; 569 AA.
AC  Q90U15:
DT  01-MAY-2000 (TrEMBLrel. 13, Created)
DT  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT  25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE  Ubiquitin ligase FWD1 (Beta-TCP protein E3RS-IkappaB) (F-box-WD40
DE  repeat protein 1) (Beta-transducin repeat containing protein).
CN  Name=Brc; Synonyms=Bxw1;
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=99199275; PubMed=10097128; DOI=10.1073/pnas.96.7.3859;
RA  Hatakeyama S., Kitagawa M., Nakayama K., Shitane M., Matsumoto M.,
RA  Hatton K., Higashi H., Nakano H., Okumura K., Ono K., Good R.A.,
RA  Nakayama K.-I.;
RT  "Ubiquitin-dependent degradation of IkappaBalpha is mediated by a

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RT  ubiquitin ligase Skp1/Cul 1/F-box protein FWD1.";
RL  Proc. Natl. Acad. Sci. U.S.A. 96:3859-3863(1999).
RN  [2]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=99075339; PubMed=9859996; DOI=10.1038/25159;
RA  Yaron A., Hatzubai A., Davis M., Lavon I., Amit S., Manning A.M.,
RA  Andersen J.S., Mann M., Mercurio F., Ben-Neriah Y.;
RT  "Identification of the receptor component of the IkappaBalpha-
RT  ubiquitin ligase.";
RN  Nature 396:590-594(1998).
RN  [3]
RP  SEQUENCE FROM N.A.
RC  STRAIN=129/Sv;
RX  MEDLINE=21601157; PubMed=11735228; DOI=10.1006/geno.2001.6658;
RA  Maruyama S., Hatakeyama S., Nakayama K., Ishida N., Kawakami K.,
RA  Nakayama K.-I.;
RT  "Characterization of a mouse gene (Bbxw6) that encodes a homologue of
RT  Caenorhabditis elegans SEL-10.";
RL  Genomics 78:214-222(2001).
RN  [4]
RP  SEQUENCE FROM N.A.
RC  STRAIN=CZECH II; TISSUE=Mammary tumor;
RX  MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA  Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA  Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA  Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA  Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
RA  Diatchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,
RA  Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA  Brownstein M.J., Uedl T.B., Toshlyuk S., Carninci P., Prange C.,
RA  Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA  Boesk S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA  Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA  Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA  Fahy J., Hellon E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA  Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA  Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA  Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA  Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schen J.E.,
RA  Jones S.J., Maria M.A.;
RT  "Generation and initial analysis of more than 15,000 full-length human
RT  and mouse cDNA sequences.";
RL  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN  [5]
RP  SEQUENCE FROM N.A.
RC  STRAIN=CZECH II; TISSUE=Mammary tumor;
RA  Strausberg R.;
RL  Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.
CC  -1- SIMILARITY: Contains 7 WD repeats.
DR  EMBL, AF081887; AAD17755.1; -
DR  EMBL, AF099932; AAD08701.1; -
DR  EMBL, AF391190; AAL40929.1; -
DR  EMBL, AF391178; AAL40929.1; JOINED.
DR  EMBL, AF391179; AAL40929.1; JOINED.
DR  EMBL, AF391183; AAL40929.1; JOINED.
DR  EMBL, AF391184; AAL40929.1; JOINED.
DR  EMBL, AF391185; AAL40929.1; JOINED.
DR  EMBL, AF391186; AAL40929.1; JOINED.
DR  EMBL, AF391187; AAL40929.1; JOINED.
DR  EMBL, AF391188; AAL40929.1; JOINED.
DR  EMBL, AF391189; AAL40929.1; JOINED.
DR  EMBL, BC003989; AAL03989.1; -
DR  HSSP, Q9Y297; 1P22.
DR  MGD, MGI:133871; Brc.
DR  GO, GO:0016874; F-ligase activity; IEA.
DR  InterPro, IPR001810; F-box.
DR  InterPro, IPR01680; WD40.
DR  InterPro, IPR01046; WD40-like.
DR  Pfam, PF00646; F-box; 1.
DR  Pfam, PF00400; WD40; 7.

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DR PRINTS: PR00320; GPROTEINBRPT.
DR ProDom: PD000018; WD40; 4.
DR SMART; SM00256; FBOX; 1.
DR SMART; SM00320; WD40; 7.
DR PROSITE; PS50181; FBOX; 1.
DR PROSITE; PS00678; WD_REPEATS_1; 6.
DR PROSITE; PS50082; WD_REPEATS_2; 7.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
DR LIGASE; Repeat; WD repeat.
KM SEQUENCE 569 AA; 65105 MW; BC7D6544815B2296 CRC64;

Query Match          98.8%; Score 2997; DB 2; Length 569;
Best Local Similarity 98.6%; Pred. No. 5,1e-217;
Matches 561; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 MDPAAVLQEKALKFNMSEREDCNGEPKRIIPKNSLRQTYNSCARCLINQETVCLA 60
DB 1 MDPAAVLQEKALKFNMSEREDCNGEPKRIIPKNSLRQTYNSCARCLINQETVCLT 60

QY 61 STAKTEKCAKTKLANGTSMIVPKORKLSASYEKEKELCVKFFQWSSSDQVEFVEHL 120
DB 61 STAKTEKCAKAKLANGTSMIVPKORKLSASYEKEKELCVKFFQWSSSDQVEFVEHL 120

QY 121 ISQCHYQHGHINSYLKPMLODFITLPAAGLDHIAENILSYLDAKSLCAAEIVCKEMY 180
DB 121 ISQCHYQHGHINSYLKPMLODFITLPAAGLDHIAENILSYLDAKSLCAAEIVCKEMY 180

QY 181 RVTSDGMLMKKLIERRMVRTSLMRGLAERRGQGYLFKNKPPDGNAPNSFYRALYPKII 240
DB 181 RVTSDGMLMKKLIERRMVRTSLMRGLAERRGQGYLFKNKPPDENAPNSFYRALYPKII 240

QY 241 ODIEETISNRCGHSIORHCHRETSKGYVCLQYDQKIVSGLRDNTIKIMDKNTLECK 300
DB 241 ODIEETISNRCGHSIORHCHRETSKGYVCLQYDQKIVSGLRDNTIKIMDKNTLECK 300

QY 301 RILGHTGSVLCLQYDERVIIITGSSDSTVRWVDVNTGEMLNTLIHCEAVLHLRFNNGM 360
DB 301 RILGHTGSVLCLQYDERVIIITGSSDSTVRWVDVNTGEMLNTLIHCEAVLHLRFNNGM 360

QY 361 VTGSKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDKKYIVSAGDRTIKWNTSTC 420
DB 361 VTGSKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDKKYIVSAGDRTIKWNTSTC 420

QY 421 EFVRTLNGHKRGIAQLQYRDLVVGSSDNTIRLMDIECGACLRVLEGHEELVRCIRPDN 480
DB 421 EFVRTLNGHKRGIAQLQYRDLVVGSSDNTIRLMDIECGACLRVLEGHEELVRCIRPDN 480

QY 481 KRIVSGAYDGKIKWMDLVAALDPRAPAGTLCRLTVHSGRVFRLQDFQIVSSSHDT 540
DB 481 KRIVSGAYDGKIKWMDLVAALDPRAPAGTLCRLTVHSGRVFRLQDFQIVSSSHDT 540

QY 541 ILIWDPLNDPAQAEPSPSPRTTYISR 569
DB 541 ILIWDPLNDPAQAEPSPSPRTTYISR 569

RESULT 3
Q92159 PRELIMINARY; PRT; 569 AA.
ID Q92159;
AC Q92159;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Beta-transducin repeat containing protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99145465; PubMed=9990853;
RA Spencer E., Jiang J., Chen Z.J.;

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RT "Signal-induced ubiquitination of IkappaBalpha by the F-box protein
RT S1mb/beta-Trcp.";
RL Genes Dev. 13:284-294(1999).
CC -1- Similarity: Contains 7 WD repeats.
DR EMBL; AF112979; AAD04181.1; -.
DR HSSP; Q9Y297; 1P22.
DR MGD; MGI:1338871; Btrc.
DR InterPro; IPR001810; F-box.
DR InterPro; IPR001680; WD40.
DR InterPro; IPR011046; WD40_Like.
DR Pfam; PF00646; F-box; 1.
DR Pfam; PF00400; WD40; 7.
DR PRINTS; PR00320; GPROTEINBRPT.
DR ProDom; PD000018; WD40; 4.
DR SMART; SM00256; FBOX; 1.
DR SMART; SM00320; WD40; 7.
DR PROSITE; PS50181; FBOX; 1.
DR PROSITE; PS00678; WD_REPEATS_1; 6.
DR PROSITE; PS50082; WD_REPEATS_2; 7.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
DR Repeat; WD repeat.
KM SEQUENCE 569 AA; 65047 MW; BC7C7A44815BED96 CRC64;

Query Match          98.5%; Score 2990; DB 2; Length 569;
Best Local Similarity 98.4%; Pred. No. 1.7e-216;
Matches 560; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 MDPAAVLQEKALKFNMSEREDCNGEPKRIIPKNSLRQTYNSCARCLINQETVCLA 60
DB 1 MDPAAVLQEKALKFNMSEREDCNGEPKRIIPKNSLRQTYNSCARCLINQETVCLT 60

QY 61 STAKTEKCAKTKLANGTSMIVPKORKLSASYEKEKELCVKFFQWSSSDQVEFVEHL 120
DB 61 STAKTEKCAKAKLANGTSMIVPKORKLSASYEKEKELCVKFFQWSSSDQVEFVEHL 120

QY 121 ISQCHYQHGHINSYLKPMLODFITLPAAGLDHIAENILSYLDAKSLCAAEIVCKEMY 180
DB 121 ISQCHYQHGHINSYLKPMLODFITLPAAGLDHIAENILSYLDAKSLCAAEIVCKEMY 180

QY 181 RVTSDGMLMKKLIERRMVRTSLMRGLAERRGQGYLFKNKPPDGNAPNSFYRALYPKII 240
DB 181 RVTSDGMLMKKLIERRMVRTSLMRGLAERRGQGYLFKNKPPDENAPNSFYRALYPKII 240

QY 241 ODIEETISNRCGHSIORHCHRETSKGYVCLQYDQKIVSGLRDNTIKIMDKNTLECK 300
DB 241 ODIEETISNRCGHSIORHCHRETSKGYVCLQYDQKIVSGLRDNTIKIMDKNTLECK 300

QY 301 RILGHTGSVLCLQYDERVIIITGSSDSTVRWVDVNTGEMLNTLIHCEAVLHLRFNNGM 360
DB 301 RILGHTGSVLCLQYGERVIIITGSSDSTVRWVDVNTGEMLNTLIHCEAVLHLRFNNGM 360

QY 361 VTGSKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDKKYIVSAGDRTIKWNTSTC 420
DB 361 VTGSKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDKKYIVSAGDRTIKWNTSTC 420

QY 421 EFVRTLNGHKRGIAQLQYRDLVVGSSDNTIRLMDIECGACLRVLEGHEELVRCIRPDN 480
DB 421 EFVRTLNGHKRGIAQLQYRDLVVGSSDNTIRLMDIECGACLRVLEGHEELVRCIRPDN 480

QY 481 KRIVSGAYDGKIKWMDLVAALDPRAPAGTLCRLTVHSGRVFRLQDFQIVSSSHDT 540
DB 481 KRIVSGAYDGKIKWMDLVAALDPRAPAGTLCRLTVHSGRVFRLQDFQIVSSSHDT 540

QY 541 ILIWDPLNDPAQAEPSPSPRTTYISR 569
DB 541 ILIWDPLNDPAQAEPSPSPRTTYISR 569

RESULT 4
Q9R1G7 PRELIMINARY; PRT; 569 AA.
ID Q9R1G7;
AC Q9R1G7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)

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DT 01-MAY-2000 (TrEMBLrel. 13, last sequence update)
DT 01-MAY-2004 (TrEMBLrel. 26, last annotation update)
DE Beta-transducin repeat-containing protein.
GN Name=Btrc;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Winston J., Elledge S.J., Harper J.W.;
RC Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 7 WD repeats.
DR EMBL; AF10396; AAD41025.1; -.
DR HSSP; O9Y297; 1P22.
DR MGD; MGI:1338871; Btrc.
DR InterPro; IPR001810; F-box.
DR InterPro; IPR001680; WD40.
DR InterPro; IPR011046; WD40_1like.
DR Pfam; PF00646; F-box; 1.
DR Pfam; PF00400; WD40; 7.
DR PRINTS; PR00320; GPROTEINBRPT.
DR ProDom; PD000018; WD40; 4.
DR SMART; SM00256; FBOX; 1.
DR SMART; SM00320; WD40; 7.
DR PROSITE; PS50181; FBOX; 1.
DR PROSITE; PS00678; WD_REPEATS_1; 6.
DR PROSITE; PS50082; WD_REPEATS_2; 7.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
KW Repeat; WD repeat.
SQ SEQUENCE 569 AA; 65209 MW; E6DDCAD28D51D9D CRC64;

Query Match 98.2%; Score 2978; DB 2; Length 569;
Best Local Similarity 97.9%; Pred. No. 1.4e-215;

Matches 557; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 MDPAAVLOEAKLKFNSSEREDCNNGEPKRIIPKNSLRQTVNSCARLCINQETVCL 60
DB 1 MDPAAVLOEAKLKFNSSEREDCNNGEPKRIIPKNSLRQTVNSCARLCINQETVCL 60
QY 61 STAMKTENCVAATKLANGTSSMIVPKORKLSASYEKEKELCVYFPEWSESQVEFEV 120
DB 61 STAMKTENCVAATKLANGTSSMIVPKORKLSASYEKEKELCVYFPEWSESQVEFEV 120
QY 121 ISOMCHYQGHINSYKPMLOQDFITLALPARGLDHTENILSYLAKSCAELVCKEY 180
DB 121 ISOMCHYQGHINSYKPMLOQDFITLALPARGLDHTENILSYLAKSCAELVCKEY 180
QY 181 RYTSQDMLMKKLIERNVRTDSLWRGLAERBGQYLFKKPPDGNAPRNSFYRALYPKII 240
DB 181 RYTSQDMLMKKLIERNVRTDSLWRGLAERBGQYLFKKPPDGNAPRNSFYRALYPKII 240
QY 241 QDIETIESNMRGSRHSLQRIHCRSETSKGVYCLQYDQKIVSGLRDNITIKIWDKNTLECK 300
DB 241 QDIETIESNMRGSRHSLQRIHCRSETSKGVYCLQYDQKIVSGLRDNITIKIWDKNTLECK 300
QY 301 RLTLGHTGSVLCIQYDERVIITGSSSDSYTRVWDVNAEMLDLTHHCEAVLHLRFNNGM 360
DB 301 RLTLGHTGSVLCIQYDERVIITGSSSDSYTRVWDVNAEMLDLTHHCEAVLHLRFNNGM 360
QY 361 VTCSKDRSLAVWDMASPTDITLRRVYVGHRAAVNVDPDKYIVASGGRITKWNNTSIC 420
DB 361 VTCSKDRSLAVWDMASPTDITLRRVYVGHRAAVNVDPDKYIVASGGRITKWNNTSIC 420
QY 421 EFVRLTLNGHKGRIACIQYDRDLVSSGSSDNTIRLMDIEGACILRVLEGHEELVRCIRPDN 480
DB 421 EFVRLTLNGHKGRIACIQYDRDLVSSGSSDNTIRLMDIEGACILRVLEGHEELVRCIRPDN 480
QY 481 KRIIVGAVYCKIKWMDIVVALDPRAAGTLCRTLVEHSGRFRLOFDFQIVSSSHDT 540
DB 481 KRIIVGAVYCKIKWMDIVVALDPRAAGTLCRTLVEHSGRFRLOFDFQIVSSSHDT 540
QY 541 ILIWDPLNDPAQAEPSPRSRTYTYISR 569

DB 541 ILIWDPLNDPAQAEPSPRSRTYTYISR 569

RESULT 5
ID 068DS0 PRELIMINARY; PRT; 564 AA.
AC 068DS0;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, last sequence update)
DE Hypothetical protein DKFZp781N011.
GN Name=DKFZp781N011;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=amygdala;
RG The German cDNA Consortium;
RA Koerner K., Beyer A., Mewes H.W., Weil B., Amid C., Oanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 7 WD repeats.
DR EMBL; CR749295; CAH18150.1; -.
DR InterPro; IPR001810; F-box.
DR InterPro; IPR001680; WD40.
DR InterPro; IPR011046; WD40_1like.
DR Pfam; PF00646; F-box; 1.
DR Pfam; PF00400; WD40; 7.
DR PRINTS; PR00320; GPROTEINBRPT.
DR ProDom; PD000018; WD40; 4.
DR SMART; SM00256; FBOX; 1.
DR SMART; SM00320; WD40; 7.
DR PROSITE; PS50181; FBOX; 1.
DR PROSITE; PS00678; WD_REPEATS_1; 6.
DR PROSITE; PS50082; WD_REPEATS_2; 7.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Hypothetical protein; Repeat; WD repeat.
KW Repeat; WD repeat.
SQ SEQUENCE 564 AA; 64201 MW; 5CCFOA7C5A59B5C1 CRC64;

Query Match 93.0%; Score 2821; DB 2; Length 564;
Best Local Similarity 100.0%; Pred. No. 8.9e-204;

Matches 528; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 QTVNSCARLCINQETVCLASTAMKTENCVAATKLANGTSSMIVPKORKLSASYEKEKELC 101
DB 37 QTVNSCARLCINQETVCLASTAMKTENCVAATKLANGTSSMIVPKORKLSASYEKEKELC 96
QY 102 VKYFPEWSESQVEFEVHELISOMCHYQGHINSYKPMLOQDFITLALPARGLDHTAENIL 161
DB 97 VKYFPEWSESQVEFEVHELISOMCHYQGHINSYKPMLOQDFITLALPARGLDHTAENIL 156
QY 162 SYLDKSLCAELVCKEYRVTSDGLMKKLIERNVRTDSLWRGLAERBGQYLFKKPP 221
DB 157 SYLDKSLCAELVCKEYRVTSDGLMKKLIERNVRTDSLWRGLAERBGQYLFKKPP 216
QY 222 PDGNAPRNSFYRALYPKIIDIETIESNMRGSRHSLQRIHCRSETSKGVYCLQYDQKIV 281
DB 217 PDGNAPRNSFYRALYPKIIDIETIESNMRGSRHSLQRIHCRSETSKGVYCLQYDQKIV 276
QY 277 SGLRDNITIKIWDKNTLECKRIITLGHGTSVLCIYDERVIITGSSSDSYTRVWDVNTGEMLN 341
DB 262 SGLRDNITIKIWDKNTLECKRIITLGHGTSVLCIYDERVIITGSSSDSYTRVWDVNTGEMLN 341
QY 342 TLIIHCEAVLHLRFNNGMVTCSKDRSLAVWDMASPTDITLRRVYVGHRAAVNVDPDK 401
DB 277 SGLRDNITIKIWDKNTLECKRIITLGHGTSVLCIYDERVIITGSSSDSYTRVWDVNTGEMLN 336
QY 337 TLIIHCEAVLHLRFNNGMVTCSKDRSLAVWDMASPTDITLRRVYVGHRAAVNVDPDK 396
DB 402 YIVSASGGRITKWNNTSICFVRLTLNGHKGRIACIQYDRDLVSSGSSDNTIRLMDIEGCA 461
DB 397 YIVSASGGRITKWNNTSICFVRLTLNGHKGRIACIQYDRDLVSSGSSDNTIRLMDIEGCA 456

Oy	46Z	CLRVLEGEHELVRRCRPEPNKRTVSGAYGCKTKWMLVAALBPRAAGTLCLRTLVHSGR	521
Db	457	CLRVLEGEHELVRRCRPFNKRITVSGAYGCKTKWMLVAALBPRAAGTLCLRTLVHSGR	516
Oy	522	VFRLOPDEFQIVSSSHDDTILIMDLPLNPAAQAEPSPRSRTYTYISR	569
Db	517	VFRLOPDEFQIVSSSHDDTILIMDLPLNPAAQAEPSPRSRTYTYISR	564

RESULT 6

ID	TRCH_XENLA	STANDARD:	PRT:	518 AA.
AC	Q91854:P70037.P70038,			
DT	15-JUL-1998 (Rel. 36, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Beta-trCP (Beta-transducin repeat-containing protein).			
GN	Name=FBXW1; Synonyms=BTRCP;			
OS	Xenopus laevis (African clawed frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;			
OC	Xenopodinae; Xenopus.			
OX	NCBI_TaxID=83355;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=93330289; PubMed=8393141;			
RA	Speak W., Keiper B.D., Stratowa C., Castranon M.J.;			
RT	"Saccharomyces cerevisiae cdc13 mutants arrested at a late stage in			
RT	anaphase are rescued by Xenopus CDNA's encoding N-ras or a protein with			
RL	beta-transducin repeats.";			
RL	Mol. Cell. Biol. 13:4953-4966(1993).			
RP	[2]			
RP	SEQUENCE OF 302-518 FROM N.A.			
RX	MEDLINE=97109804; PubMed=8952061;			
RX	DOI=10.1002/(SICI)1520-6408(1996)19:3<190::AID-DVG2>3.3.CO;2-Y;			
RA	Hudson J.W., Alarcon V.B., Elinson R.P.;			
RT	"Identification of new localized RNAs in the Xenopus oocyte by			
RT	differential display PCR.";			
RL	Dev. Genet. 19:190-198(1996).			
CC	-I- FUNCTION: Probably recognizes and binds to some phosphorylated			
CC	proteins and promotes their ubiquitination and degradation. May			
CC	participate in Mit signaling.			
CC	-I- SUBUNIT: Part of a SCF (SKR1-cullin-F-box) protein ligase complex			
CC	(By similarity).			
CC	-I- DEVELOPMENTAL STAGE: Present in fully grown and progesterone-			
CC	matured oocytes. The level change very little even after zygotic			
CC	gene transcription begins following the midblastula transition. Do			
CC	not increase in abundance in the gastrula, neurula, tailbud, or			
CC	tadpole embryo.			
CC	-I- SIMILARITY: Contains 1 F-box domain.			
CC	-I- SIMILARITY: Contains 7 WD repeats.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation			
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CC	or send an email to licenses@isb-sdb.ch).			
CC	-----			
DR	EMBL; M98268; AAA02810.1; -			
DR	EMBL; U63921; AAB49671.1; -			
DR	EMBL; U63922; AAB49672.1; -			
DR	PIR; B48088; B48088.			
DR	HSIP; Q9Y297; 1P22.			
DR	InterPro; IPR001810; F-box.			
DR	InterPro; IPR008945; Skp1_Skp2.			
DR	InterPro; IPR001680; WD40_			
DR	InterPro; IPR011046; WD40_like.			
DR	Pfam; PF00646; F-box_1.			
DR	Pfam; PF00400; WD40_7.			
DR	PRINTS; PR00320; GPROTEINBRPT.			

Query Match	Best Local Similarity	85.6%; Score 2597; DB 1; Length 518;
Matches 488; Conservative 7; Mismatches 8; Indels 30; Gaps 1;		
DR PRODOM;P0000018; WD40; 4.		
DR SMART; SMO0256; FBOX; 1.		
DR SMART; SMO0320; WD40; 7.		
DR PROSITE; PS00181; FBOX; 1.		
DR PROSITE; PS00678; WD_REPEATS 1; 6.		
DR PROSITE; PS00824; WD_REPEATS 2; 7.		
DR PROSITE; PS050294; WD_REPEATS_REGION; 1.		
KW Repeat; Db1 conjugation pathway; WD repeat; Wnt signaling pathway.		
FT DOMAIN	119	157
FT REPEAT	230	258
FT REPEAT	270	298
FT REPEAT	310	338
FT REPEAT	353	381
FT REPEAT	393	421
FT REPEAT	433	461
FT REPEAT	482	510
FT CONFLICT	302	304
FT CONFLICT	516	518
SEQUENCE	518 AA; 59507 MM; 2A52EC19028127F5 CRC64;	
Query Match	85.6%; Score 2597; DB 1; Length 518;	
Best Local Similarity	91.6%; Pred. No. 5,8e-187;	
Matches 488; Conservative 7; Mismatches 8; Indels 30; Gaps 1;		
OY 18 SSEDNCNGEPKKIIPKSKLSQTNASCARLCLNQETVCLASTAMKTENCVAKTIAN 77		
DB 13 ASEREDCNREBPPIKTIETKNTLQ-----TKLAN 42		
OY 78 GTSMIVPKOKLSASYEKEKELCVKYPEOMSESDOVEFVHLISOMCHYGHINSYLK 137		
DB 43 GTSMIVPKOKLSASYEKEKELCVKYPEOMSESDOVEFVHLISOMCHYGHINSYLK 102		
OY 138 PMLQRPFTALPARGLPHIAENILSYLDAKSLCAELVCKEYVTSQDMLKKLIERNV 197		
DB 103 PMLQRPFTALPARGLPHIANILSYLDAKSLCAELVCKEYVTSQDMLKKLIERNV 162		
OY 198 RTDSLWRLGLARRGQGYLFPNKKPPDGNAPNSTFYRLPKIIDIETIESNMGCRSL 257		
DB 163 RTDSLWRLGLARRGQGYLFPNKKPPDGNAPNSTFYRLPKIIDIETIESNMGCRSL 222		
OY 258 QRHCRRSTSGVYCLQYDDQKIVSGLRDNITKIMDKNTLCKRILNGTGSVLCLOYE 317		
DB 223 QRHCRRSTSGVYCLQYDDQKIVSGLRDNITKIMDKNTLCKRILNGTGSVLCLOYE 282		
OY 318 RVITGSSDSIVRWVNTGEMLTWLIIHCQAVLHLRFNNQMMYTCSDKRSIAWDMASP 377		
DB 283 RVITGSSDSIVRWVNTGEMLTWLIIHCQAVLHLRFNNQMMYTCSDKRSIAWDMASP 342		
OY 378 TDTITLRLVVGRAAVVVPDDKXYIVSASGDRITIKWNTISTCEPFTLNGHKGIAQLQ 437		
DB 343 TDTITLRLVVGRAAVVVPDDKXYIVSASGDRITIKWNTISTCEPFTLNGHKGIAQLQ 402		
OY 438 YRDLVYSGSSDNTIRLMDIECGACRLRLBEHEELVRLIRPDNRIVSGAVDGKIKWDL 497		
DB 403 YRDLVYSGSSDNTIRLMDIECGACRLRLBEHEELVRLIRPDNRIVSGAVDGKIKWDL 462		
OY 498 VVALDPRAPATGLCLRTLVHSGVFRLOQEFQIVSSSHDITLIWFLNDP 550		
DB 463 VVALDPRAPATGLCLRTLVHSGVFRLOQEFQIVSSSHDITLIWFLNDP 515		
RESULT 7		
Q8BY90 PRELIMINARY; PRT; 529 AA.		
AC Q8BY90;		
DT 01-MAR-2003 (TREMBLrel. 23, Created)		
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)		
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)		
DE Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630019J11 product:F-box/WD-REPEAT PROTEIN 1B (F-BOX		
DE AND WD-REPEATS PROTEIN BETA-TCP2) .HOMOLOG.		
OS Name=Fdxw11; Synonyms=Fdxw1b; Mus musculus (Mouse).		

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteleia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=99227925; Pubmed=1034966; DOI=10.1016/S0076-6879(99)00004-9;
RA Carninci P., Hayashizaki Y.,
RT "High efficiency full-length cDNA cloning,"
RL Mech. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=21085660; Pubmed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection,"
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RA The RIKEN Consortium,
RT The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RL 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20499374; Pubmed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Suganaka T., Shibata K., Itoh M.,
RT Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RL prepare full-length cDNA libraries for rapid discovery of new genes,";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20530913; Pubmed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kikunai T., Tashiro H., Itoh M.,
RA Suni N., Ishi Y., Nakamura S., Hazama M., Nishino T., Harada A.,
RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kasaiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer,";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiroaka T., Hirozane T.,
RA Hori F., Imclanti K., Ishi Y., Itoh M., Kagawa I., Kusakawa T.,
RA Kachi H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
RA Kuribara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ono M., Ohsato N., Okazaki Y.,
RA Saito K., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Saeki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaki-Akhiba S., Takeda Y., Tanaka T.,
RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2001) to the EMBL/Genbank/DBSJ databases.
RN [7]
CC - SIMILARITY: Contains 7 wd repeats.
DR EMBL; AK041532; BR030975.1; -.
DR HSSP; Q9Y297; 1P22.
DR MGI; MGI:2144023; FbXw11.
DR InterPro; IPR001810; F-box.
DR InterPro; IPR001680; WD40.
DR InterPro; IPR011046; WD40_like.
DR Pfam; PF00646; F-box; 1.
DR Pfam; PF00400; WD40; 7.
DR PRINTS; PR00320; GPROTEINBPT.

Query Match	Similarity	Score	DB 2395	DB 22	Length	529
Matches 449	Conservative 43	Mismatches 37	Indels 40	Gaps 3		
DR	ProDom; P0000018; WD40; 4.					
DR	SMART; SM00256; FBOX; 1.					
DR	SMART; SM00320; WD40; 7.					
DR	PROSITE; PS0181; FBOX; 1.					
DR	PROSITE; PS00678; WD_REPEATS_1; 5.					
DR	PROSITE; PS00883; WD_REPEATS_2; 7.					
DR	PROSITE; PS50294; WD_REPEATS_REGION; 1.					
KW	Repeat; WD repeat.					
SC	SEQUENCE 529 AA; 60812 MW; D2F382457FD80080 CRC64;					
Query Match	78.9%;	Score 2395;	DB 22;	Length 529;		
Matches 449	Conservative 43	Mismatches 37	Indels 40	Gaps 3		
DR	ProDom; P0000018; WD40; 4.					
DR	SMART; SM00256; FBOX; 1.					
DR	SMART; SM00320; WD40; 7.					
DR	PROSITE; PS0181; FBOX; 1.					
DR	PROSITE; PS00678; WD_REPEATS_1; 5.					
DR	PROSITE; PS00883; WD_REPEATS_2; 7.					
DR	PROSITE; PS50294; WD_REPEATS_REGION; 1.					
KW	Repeat; WD repeat.					
SC	SEQUENCE 529 AA; 60812 MW; D2F382457FD80080 CRC64;					
DR	ProDom; P0000018; WD40; 4.					
DR	SMART; SM00256; FBOX; 1.					
DR	SMART; SM00320; WD40; 7.					
DR	PROSITE; PS0181; FBOX; 1.					
DR	PROSITE; PS00678; WD_REPEATS_1; 5.					
DR	PROSITE; PS00883; WD_REPEATS_2; 7.					
DR	PROSITE; PS50294; WD_REPEATS_REGION; 1.					
KW	Repeat; WD repeat.					
SC	SEQUENCE 529 AA; 60812 MW; D2F382457FD80080 CRC64;					
DR	ProDom; P0000018; WD40; 4.					
DR	SMART; SM00256; FBOX; 1.					
DR	SMART; SM00320; WD40; 7.					
DR	PROSITE; PS0181; FBOX; 1.					
DR	PROSITE; PS00678; WD_REPEATS_1; 5.					
DR	PROSITE; PS00883; WD_REPEATS_2; 7.					
DR	PROSITE; PS50294; WD_REPEATS_REGION; 1.					
KW	Repeat; WD repeat.					
SC	SEQUENCE 529 AA; 60812 MW; D2F382457FD80080 CRC64;					
DR	ProDom; P0000018; WD40; 4.					
DR	SMART; SM00256; FBOX; 1.					
DR	SMART; SM00320; WD40; 7.					
DR	PROSITE; PS0181; FBOX; 1.					
DR	PROSITE; PS00678; WD_REPEATS_1; 5.					
DR	PROSITE; PS00883; WD_REPEATS_2; 7.					
DR	PROSITE; PS50294; WD_REPEATS_REGION; 1.					
KW	Repeat; WD repeat.					
SC	SEQUENCE 529 AA; 60812 MW; D2F382457FD80080 CRC64;					
DR	ProDom; P0000018; WD40; 4.					
DR	SMART; SM00256; FBOX; 1.					
DR	SMART; SM00320; WD40; 7.					
DR	PROSITE; PS0181; FBOX; 1.					
DR	PROSITE; PS00678; WD_REPEATS_1; 5.					
DR	PROSITE; PS00883; WD_REPEATS_2; 7.					
DR	PROSITE; PS50294; WD_REPEATS_REGION; 1.					
KW	Repeat; WD repeat.					
SC	SEQUENCE 529 AA; 60812 MW; D2F382457FD80080 CRC64;					
DR	ProDom; P0000018; WD40; 4.					
DR	SMART; SM00256; FBOX; 1.					
DR	SMART; SM00320; WD40; 7.					
DR	PROSITE; PS0181; FBOX; 1.					
DR	PROSITE; PS00678; WD_REPEATS_1; 5.					
DR	PROSITE; PS00883; WD_REPEATS_2; 7.					
DR	PROSITE; PS50294; WD_REPEATS_REGION; 1.					
KW	Repeat; WD repeat.			</		

RA Pagano M.;
RT "Identification of a family of human F-box proteins.";
RN Curr. Biol. 9:1177-1179(1999).
[2]
RN SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RP TISSUE=Fetal lung;
RC MEDLINE=20160458; PubMed=10694485; DOI=10.1006/dbrc.2000.2241;
RX Koike J., Sagara N., Kitikoshi H., Takagi A., Miwa T., Hirai M.,
RA Katoh M.;
RT "Molecular cloning and genomic structure of the betaTRCP2 gene on
RT chromosome 5q35.1.";
RL Biochem. Biophys. Res. Commun. 269:103-109(2000).
[3]
RN SEQUENCE FROM N.A.
RP TISSUE=Brain;
RC MEDLINE=98403980; PubMed=97334811;
RX Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A.,
RA Kocani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human gene. X.
RT The complete sequences of 100 new cDNA clones from brain which can
RT code for large proteins in vitro.";
RL DNA Res. 5:169-176(1998).
[4]
RN SEQUENCE FROM N.A. (ISOFORM B).
RP TISSUE=Lymph;
RC MEDLINE=22388557; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Struhsberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmer C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marnett K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi A.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinci P., Prange C.,
RA Rahn S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosnak S.A., McGowan P.C., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hilyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.T., Skalska U., Smallus D.E.,
RA Schermer A., Schein J.E., Jones S.J.W., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[5]
CC -!- FUNCTION: Probably recognizes and binds to some phosphorylated
CC proteins and promotes their ubiquitination and degradation. May
CC participate in Wnt signaling.
CC -!- SUBUNIT: Part of a SCF (SKR1-cullin-F-box) protein ligase complex.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (potential).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=C;
CC IsoId=g9UKH1-1; Sequence=Displayed;
CC Name=A;
CC IsoId=g9UKH1-2; Sequence=VSP_006765;
CC Name=B;
CC IsoId=g9UKH1-3; Sequence=VSP_006766;
CC -!- SIMILARITY: Contains 1 F-box domain.
CC -!- SIMILARITY: Contains 7 WD repeats.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL, AF176022; AAF04528.1; -;
CC DR EMBL, AB033279; BAA92329.1; -;
CC DR EMBL, AB033280; BAA92330.1; -;

[illegible]

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DB 392 TCEPRTLNHGHRGACIACQYRDLVYSSSDNTIRIMDEICGACLRVDEGHELVKRCIF 451
QY 479 DNKRIYSGAYDGKIKYWDVVALDPAPAGTCLRTLVHSGRVFLQGFDEFOIVSSSHD 538
DB 452 DNKRIYSGAYDGKIKYWDVVALDPAPAGTCLRTLVHSGRVFLQGFDEFOIVSSSHD 511
QY 539 DTLLIMDFLNDPAPAAQAPRPSRTTYISR 569
DB 512 DTLLIMDFLNDPAPAAQAPRPSRTTYISR 542

RESULT 9
08K022 PRELIMINARY; PRT; 563 AA.
AC 08K022;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DE 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE F-box and WD-40 domain protein 11.
GN Name=Fbxw11;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Struhsberg R.L., Felting E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Boeck S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny K.C., Hale S., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimsrud J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Scherch A., Schein J.E.,
RA Jones S.J., Maier M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Kidney;
RX Submitted (JUL-2002) to the EMBL/Genbank/DBJ databases.
RA Struhsberg R.;
DE -1- SIMILARITY: Contains 7 WD repeats.
CC EMBL: BC034261; AAH34261.1; -.
DR HSSP; Q9Y297; IP22.
DR InterPro; IPR001810; F-box.
DR InterPro; IPR001680; WD40.
DR InterPro; IPR01046; WD40_1like.
DR Pfam; PF00646; F-box; 1.
DR PRINTS; PR00320; GPROTEINRPT.
DR PRODOM; PD000018; WD40_4.
DR SMART; SM00256; FBOX; 1.
DR SMART; SM00320; WD40; 7.
DR PROSITE; PS50181; FBOX; 1.
DR PROSITE; PS00678; WD_REPEATS_1; 5.
DR PROSITE; PS50082; WD_REPEATS_2; 7.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
SQ SEQUENCE 563 AA; 64481 MW; 74D07E6B850ABED CRC64;

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Query Match 78.4%; Score 2380; DB 2; Length 563;
Best Local Similarity 78.1%; Pred. No. 1.4e-170;
Matches 454; Conservative 46; Mismatches 51; Indels 30; Gaps 7;

QY 1 MDPAAVLQEKALKFNNSSERE---DNNGBPPRKIIPEKNSLRQTYNSCARCLNQ--E 55
DB 1 MDP--DSVIEDKTIELMCSVPRSLWGCAN-----LYESNCALSLQSMPS 44
QY 56 TVCLASTA-MKTEN-----CVAKTKLANGTSSMTVPKORKLSAYEKELCVKFFEW 108
DB 45 VACLQNTSVEMDQNDDESPKRSALWQISNGTSSVIVSRRRPSEGNVQKEXDKLCIKYFDW 104
QY 109 SESDQVEFVEHLISQMCYOHGHINSYLPKMQRPDFTALPARGLHIAENILSYLDAS 168
DB 105 SESDQVEFVEHLISQMCYOHGHINSYLPKMQRPDFTALPARGLHIAENILSYLDAS 164
QY 169 LCAAEVLCKEYRYVTSQGLMWKGLIERVVRTDSLWRGLAERRGQVLEPKNPPGNAP 228
DB 165 LCAAEVLCKEYRYVTSQGLMWKGLIERVVRTDPLWKGLSERGMDQVLEPKNPTDG--PP 222
QY 229 NSFYRALPKTIQDIETTESNWRCCGRHSQRHCHGSEFSKTYCYQYDDOKIVSGLRDT 288
DB 223 NSFYSILPKTIQDIETTESNWRCCGRHNLQRHCHGSEFSKTYCYQYDDOKIVSGLRDT 282
QY 289 IKIMDKNTLECKRILTGHGTVLCTQYDERVITGSSDSQTVRVMVDNGEMTLIHCE 348
DB 283 IKIMDKNTLECKRILTGHGTVLCTQYDERVITGSSDSQTVRVMVDNGEMTLIHCE 342
QY 349 AVTLHLRFNNGMVNTCSKORSIAVWDMASPTDITLRLVYVGHRAAVNVVDFDDKTVSASG 408
DB 343 AVTLHLRFNSGLMNTCSKORSIAVWDMASPTDITLRLVYVGHRAAVNVVDFDDKTVSASG 402
QY 409 DRTIVVNTSTGEFRTLNHGHRGACIACQYRDLVYSSSDNTIRIMDEICGACLRVLEG 468
DB 403 DRTIVVNTSTGEFRTLNHGHRGACIACQYRDLVYSSSDNTIRIMDEICGACLRVLEG 462
QY 469 HEELVRCRFPDKRIVSGAYDGKIKYWDVVALDPAPAGTCLRTLVHSGRVFLQDP 528
DB 463 HEELVRCRFPDKRIVSGAYDGKIKYWDVVALDPAPAGTCLRTLVHSGRVFLQDP 522
QY 529 EFQIVSSSHDDTLLIMDFLNDPAPAAQAPRPSRTTYISR 569
DB 523 EFQIVSSSHDDTLLIMDFLNDPAPAAQAPRPSRTTYISR 563

RESULT 10
08CHDS PRELIMINARY; PRT; 555 AA.
AC 08CHDS;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DE 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE MKIAA0696 protein (Fragment).
GN Name=Fbxw11; Synonyms=Fbxw1b, MKIAA0696;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Hara Y., Nagase T.,
RA Ohara O., Koga H.;
RX Submitted (Oct-2002) to the EMBL/Genbank/DBJ databases.
DE -1- SIMILARITY: Contains 7 WD repeats.
CC EMBL: AB093260; BAC1444.1; -.
DR HSSP; Q9Y297; IP22.
DR MGI; MGI:2144023; Fbxw11.
DR InterPro; IPR001810; F-box.
DR InterPro; IPR001680; WD40.
DR InterPro; IPR01046; WD40_1like.
DR Pfam; PF00646; F-box; 1.
DR Pfam; PF00400; WD40; 7.

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DR PRINTS; PR00320; GPROTEINBRPT.
DR Prodom; PD000018; WD40; 4.
DR SMART; SM00256; FBOX; 1.
DR SMART; SM00320; WD40; 7.
DR PROSITE; PS50181; FBOX; 1.
DR PROSITE; PS00678; WD_REPEATS_1; 5.
DR PROSITE; PS50082; WD_REPEATS_2; 7.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KM Repeat; WD repeat.
FT NON_TER 1
SQ SEQUENCE 555 AA; 63287 MW; 6052496DACA489 CRC64;

Query Match
Best Local Similarity 81.9%; Score 2360; DB 2; Length 555;
Matches 443; Conservative 38; Mismatches 46; Indels 14; Gaps 3;

OY 29 PERKIIPEKNSLRQTYNSCARCLNQETVCLASTAMKTENCVAKTKLANGTSSMTVPKOR 88
DB 29 PPGPIAAE---RRRRGGAAGAAMPDSV-----IEDKTIELMISNGTSVIVSRKR 76
OY 89 KLSASYEKKEKLCVQYFEQMSSDQVEFEHLISQMHYQGHINSYKPKMLQRPFTAL 148
DB 77 PSEGVYQKEKDCITYFQWSSSDQVEFEHLISQMHYQGHINSYKPKMLQRPFTAL 136
OY 149 PARGLDHAENILSYLDAKSLCAAEIVCKEYRYVSDGMLMKKLIERNVTRDLSLRGLAE 208
DB 137 PEQGLDHAENILSYLDAKSLCAAEIVCKEYRYVSDGMLMKKLIERNVTRDLSLRGLAE 196
OY 209 RRGWQOYLFEKNRPDGNAPPNPSFYAPYKIIQDIETIESNMRCGRHSIQRIHCRSETSK 268
DB 197 RRGWQOYLFEKNRPDGNAPPNPSFYAPYKIIQDIETIESNMRCGRHSIQRIHCRSETSK 254
OY 269 GYVCIQYDDOKIVSGLRDNTIKIMDKNTIECKRIITGHTGSVLCIQYDERVITVSSSST 328
DB 255 GYVCIQYDDOKIVSGLRDNTIKIMDKNTIECKRIITGHTGSVLCIQYDERVITVSSSST 314
OY 329 VAVMDVNTGEMLNTLIHCEAVLHLPFNNGMVAVTCSDRSIAVMDMASPTDITLRRVAVG 388
DB 315 VAVMDVNTGEMLNTLIHCEAVLHLPFNNGMVAVTCSDRSIAVMDMASPTDITLRRVAVG 374
OY 389 HRAAVNVVDFDDKYIVSASGDRITIKVNTSTCEPVRTLNGHRRGIACIQYDRDLVVGSS 448
DB 375 HRAAVNVVDFDDKYIVSASGDRITIKVNTSTCEPVRTLNGHRRGIACIQYDRDLVVGSS 434
OY 449 DNTITLMDIEGCACLRVLEGHELVRCIRFDNKRIVSGAYDGKIKVMDLQALDPRAPAS 508
DB 435 DNTITLMDIEGCACLRVLEGHELVRCIRFDNKRIVSGAYDGKIKVMDLQALDPRAPAS 494
OY 509 TLCLRTLVHSGRVFLQDFEQIVSSSHDDTILIMDFLNDPAQAEPSPRSRTTYIYS 568
DB 495 TLCLRTLVHSGRVFLQDFEQIVSSSHDDTILIMDFLNDPAQAEPSPRSRTTYIYS 554
OY 569 R 569
DB 555 R 555

RESULT 11
O923HO PRELIMINARY; PRT; 563 AA.
AC Q923HO;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
F-box/WD40 repeat-containing protein HOS.
Name=Fbxw11; Synonyms=Fbxw1b;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OK NCBI_TaxId=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N;

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RX MEDLINE=21906231; PubMed=11896578; DOI=10.1038/sj.onc.1205311;
RA Bhatia N., Herter J.R., Slaga T.J., Fuchs S.Y., Spigelman V.S.;
RT "Mouse homologue of HOS (mHOS) is overexpressed in skin tumors and
RT implicated in constitutive activation of NF-kappaB.";
RL Oncogene 21:1501-1509(2002).
CC -1 SIMILARITY: Contains 7 wd repeats.
DR EMBL; AY038079; AAK72095.1; -.
DR HSSP; O9Y297; 1p22.
DR MGI; MGI:2144023; Fbxw11.
DR Pfam; PF00646; F-box; 1.
DR Pfam; PF00400; WD40; 7.
DR PRINTS; PR00320; GPROTEINBRPT.
DR Prodom; PD000018; WD40; 4.
DR SMART; SM00256; FBOX; 1.
DR SMART; SM00320; WD40; 7.
DR PROSITE; PS50181; FBOX; 1.
DR PROSITE; PS00678; WD_REPEATS_1; 5.
DR PROSITE; PS50082; WD_REPEATS_2; 7.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KM Repeat; WD repeat.
SQ SEQUENCE 563 AA; 64741 MW; 9AB562F3FF5E3496 CRC64;

Query Match
Best Local Similarity 75.3%; Score 2286; DB 2; Length 563;
Matches 440; Conservative 46; Mismatches 65; Indels 30; Gaps 7;

OY 1 MDPKAVLQGEALKFNNSSRE---DGNNGEPKKIIPKNSLRQTYNSCARCLNQ--E 55
DB 1 MEP-DVIEDTETIELMCSVPISLMLGCAN-----LVSMCLSLCQSMPS 44
OY 56 TVCLASTA-MKTEN-----CVAKTKLANGTSSMTVPKORKLASAYEKKEKLCVQYFEQW 108
DB 45 VRCIONTNVWEDQNBEDSPKKSALMOISNGSSVIVSRKRPSEBNYQKEKDCITYFQW 104
OY 109 SESDQVEFEHLISQMHYQGHINSYKPKMLQRPFTALPARGLDHAENILSYLDAKS 168
DB 105 SESDQVEFEHLISQMHYQGHINSYKPKMLQRPFTALPEQGLDHAENILSYLDAKS 164
OY 169 LCAAEIVCKEYRYVSDGMLMKKLIERNVTRDLSLRGLARRGGQYLFKNRPDGNAPP 228
DB 165 LCAAEIVCKEYRYVSDGMLMKKLIERNVTRDLSLRGLARRGGQYLFKNRPDGNAPP 222
OY 229 NSFAYALPYKIIQDIETIESNMRCGRHSIQRIHCRSETSKGVYLCIQYDDOKIVSGLRDNT 288
DB 223 NSFAYALPYKIIQDIETIESNMRCGRHSIQRIHCRSETSKGVYLCIQYDDOKIVSGLRDNT 282
OY 289 IKIMDKNTIECKRIITGHTGSVLCIQYDERVITVSSSSTVYRWDVNTGEMLNTLIHCE 348
DB 283 IKIMDKNTIECKRIITGHTGSVLCIQYDERVITVSSSSTVYRWDVNTGEMLNTLIHNE 342
OY 349 AVLHLRFPNGMVAVTCSDRSIAVMDMASPTDITLRRVAVGHRAAVNVVDFDDKYIVSASG 408
DB 343 AVLHLRFPNGMVAVTCSDRSIAVMDMASPTDITLRRVAVGHRAAVNVVDFDDKYIVSASG 402
OY 409 DRTIKVNTSTCEPVRTLNGHRRGIACIQYDRDLVVGSSSDNTIRLMDIEGCACLRVLEG 468
DB 403 DRTIKVNTSTCEPVRTLNGHRRGIACIQYDRDLVVGSSSDNTIRLMDIEGCACLRVLEG 462
OY 469 HEELVRCIRFDNKRIVSGAYDGKIKVMDLQALDPRAPAGTLCRTLVHSGRVFLQDF 528
DB 463 HEELVRCIRFDNKRIVSGAYDGKIKVMDLQALDPRAPASTLCRTLVHSGRVFLQDF 522
OY 529 EFOIVSSSHDDTILIMDFLNDPAQAEPSPRSRTTYIYS 569
DB 523 EFOIVSSSHDDTILIMDFLNDPAQAEPSPRSRTTYIYS 563

RESULT 12
O6PGM4 PRELIMINARY; PRT; 527 AA.
AC O6PGM4;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)

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DT 05-JUL-2004 (TrEMBLrel. 27, last annotation update)
 DE Zgc:63728.
 GN ORFNames=zgc:63728;
 OS Brachydanio rerio (zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 NCBI_Taxid=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AB; TISSUE=whole body;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stabileton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loguellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Maier M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AB; TISSUE=whole body;
 RX Strausberg R.;
 RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 7 WD repeats.
 DR EMBL, BC056809; AAH56809.1; -;
 DR ZFIN, ZDB-GENE-040426-2903; zgc:63728.
 DR InterPro; IPR001810; F-box.
 DR InterPro; IPR010680; WD40.
 DR InterPro; IPR011046; WD40_1like.
 DR Pfam; PF00646; F-box; 1.
 DR Pfam; PF00400; WD40; 7.
 DR PRINTS; PR00320; GPROTEINRPT.
 DR PRODom; PD000018; WD40; 4.
 DR SMART; SM00256; FBOX; 1.
 DR SMART; SM00320; WD40; 7.
 DR PROSITE; PSS0181; FBOX; 1.
 DR PROSITE; PSS00678; WD_REPEATS_1; 5.
 DR PROSITE; PSS00882; WD_REPEATS_2; 7.
 DR PROSITE; PSS0294; WD_REPEATS_REGION; 1.
 DR Repeat; WD repeat.
 SQ SEQUENCE 527 AA; 60546 MW; 563F3C014CA099C3 CRC64;
 Query Match 74.4%; Score 2258.5; DB 2; Length 527;
 Best Local Similarity 76.1%; Pred. No. 1.8e-161;
 Matches 430; Conservative 49; Mismatches 45; Indels 41; Gaps 6;
 QY 8 LOEKALKENSSEREDCNNGEPKRIPEKSLRQTVNSCARLQNGEN-VCLASAMKT 66
 DB 1 MEDKTLQKNNISVMD- - - - - QADNSPKITLIKSTFTIC- - - - - 34
 QY 67 ENCVAKTKLANG--TSSMIVPKORKLSAYEKEKEKLCVYFPMQSSDQVEFEVHLISQM 124
 DB 35 - - - - - PQVSNGLPLTGS- - - - - KRPBEGNYEKEKQDVCIGLFWGSDQDQVEFEVHLISM 84
 QY 125 CHYOHGHTNSYLKPMQORFITALPAKGLDHAENLSTLIDAKSLCAALVCKEKWRVTS 184
 DB 85 CHYOHGHTNSYLKPMQORFITALPAKGLDHAENLSTLIDAKSLCAALVCKEKWRVTS 144
 QY 185 DGLMWKLIETRWRTDSTLWRGLAERGMQGYLFKNKPPDGNAPPNPSFYALPKIIQDIE 244

DB 145 EGMWKKLIETRWRTDPLMKGLSERHQMEKYLFRKRTTE--VPPNSYNSLVPKIIQDIE 202
 QY 245 TIESNWRGCRNALQKIHCRSETSKGYVCLQYDQDKIVSLRNTTKIMKNTLECKRIIT 304
 DB 203 TIEANWRGCRNHLQRIQCRSENSKGYVCLQYDDEKISGLRDNISIKIMDKQTLCEKLIIT 262
 QY 305 GHTGSVLCIQYDERVITIGSSSDSTVRVMDVNTGEMLNTLIHHCEVLIHLRFNNGMVTC 364
 DB 263 GHTGSVLCIQYDERVITIGSSSDSTVRVMDVNSGVALNTLIHNEVLIHLRFNGLAVTOS 322
 QY 365 KDRSLAVMDMASPTDITLRVLVGRRAAVNVDPDKIVSASGDRITIKVNTSTCEFYR 424
 DB 323 KDRSLAVMDMASPTDITLRVLVGRRAAVNVDPDKIVSASGDRITIKVNTSTCEFYR 382
 QY 425 TLNGHKRGIAQLQYDRILVSGSSDNTIRLMDIEGACILRVLEGHELVRCIRPDNRIV 484
 DB 383 TLNGHKRGIAQLQYDRILVSGSSDNTIRLMDIEGACILRVLEGHELVRCIRPDNRIV 442
 QY 485 SGAYNGKIKVMDLVAALDPRAAGTLCRTVYHSGRVPRLOPDFQVSSSHDPTILW 544
 DB 443 SGAYNGKIKVMDLQALDPRAASTLCRTVYHSGRVPRLOPDFQVSSSHDPTILW 502
 QY 545 DEIANDPAQAEBPPRSRPTTYISR 569
 DB 503 DEIANDPAQAEBPPRSRPTTYISR 527
 RESULT 13
 Q7ZVZ1
 ID 07ZVZ1 PRELIMINARY; PRT: 527 AA.
 AC 07ZVZ1;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, last annotation update)
 DE F-box and WD-40 domain protein 1B.
 GN Name=fbxwb;
 OS Brachydanio rerio (zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 NCBI_Taxid=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AB; TISSUE=whole body;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stabileton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loguellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Maier M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AB; TISSUE=whole body;
 RX Strausberg R.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 7 WD repeats.
 DR EMBL, BC045356; AAH45356.1; -;


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DR HSSP; Q9Y297; 1P22.  
DR ZFIN; ZDB-GENE-030131-6305; fbxwlb.  
DR InterPro; IPR001810; F-box.  
DR InterPro; IPR01680; WD40.  
DR InterPro; IPR01046; WD40_like.  
DR Pfam; PF00646; F-box; 1.  
DR Pfam; PF00400; WD40; 7.  
DR PRINTS; PR00320; GPROTEINRPT.  
DR Prodom; PD000018; WD40; 4.  
DR SMART; SM00256; FBOX; 1.  
DR SMART; SM00320; WD40; 7.  
DR PROSITE; PS50181; FBOX; 1.  
DR PROSITE; PS00678; WD_REPEATS_1; 5.  
DR PROSITE; PS50082; WD_REPEATS_2; 7.  
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.  
KW Repeat; WD repeat.  
SQ SEQUENCE 527 AA; 60365 MW; 8AB60CEBB84963DA CRC64;  
  
Query Match 74.2%; Score 2250; DB 2; Length 527;  
Best Local Similarity 75.0%; Pred. No. 8e-161;  
Matches 427; Conservative 49; Mismatches 51; Indels 42; Gaps 5;  
  
QY 1 MDPBAVLQERALKFENSSEREDCNNGEPKRIIEKNSLRQYNSCARLCLNDETVCLA 60  
DB 1 MDPDK---EDKTLBELMNTGMESQINTD---EVSFKTTV----- 34  
  
QY 61 STAMKTEHCVAKTAKLANGTSSMIVPKRKLSASYKEKELCVKYTFEOWSESDOVEFVH 120  
DB 35 -----FKGNG--SLAGSRKRPSSQSPKFKDLCTLPDOWSESQVEFVH 80  
  
QY 121 ISOMCHYOHGHNSTLYKPMLOQDFETALPARGLDHAENILSYDAKSLCAELVCCKEMY 180  
DB 81 IARMKHYOHGHNSTLYKPMLOQDFETALPARGLDHAENILSYDAKSLCAELVCCKEMY 140  
  
QY 181 RYTSQGLMKKLIEMRVRTSLMRGLAERRGQYLFKNKPPDGNAPNSFYRALYPKII 240  
DB 141 RYISQGLMKKLIEMRVRTSLMRGLAERRGQYLFKNR--TNEVPNSYHSLYPKII 198  
  
QY 241 ODIEETIESNNRCGRSLQRIHCRSTSKGVYCLQYDDOKIYSGLADNTIKIWDKNTLECK 300  
DB 199 ODIEETIESNNRCGRSLQRIHCRSTSKGVYCLQYDDOKIISGLADNISKIWDKNTLECK 258  
  
QY 301 RILHTGTSVLCLODERVIITGSSDSTYRVMDVNTGEMLNTLIHCEAVLHFRNNGM 360  
DB 259 KVLHTGTSVLCLODERVIITGSSDSTYRVMDVNTGEMLNTLIHCEAVLHFRNNGM 318  
  
QY 361 VTCSKORSIAVWDMASPTDITLRVLYVGHRAAVNVDPDKXIYASAGDRTIKWNTSTC 420  
DB 319 VTCSKORSIAVWDMASPTDITLRVLYVGHRAAVNVDPDKXIYASAGDRTIKWNTSTC 378  
  
QY 421 EFVRLTLNGHKGIAICLQYRDRLVSGSSDNTIRLWDIEGACLRVLEGHEELVRCIRFDN 480  
DB 379 EFVRLTLNGHKGIAICLQYRDRLVSGSSDNTIRLWDIEGACLRVLEGHEELVRCIRFDN 438  
  
QY 481 KRIYGAAYDGKIKVMDLVAALDPRAPAGTLCIRTVEHSGRVRLOPDEFQIVSSSHDT 540  
DB 439 KRIYGAAYDGKIKVMDLVAALDPRAPAGTLCIRTVEHSGRVRLOPDEFQIVSSSHDT 498  
  
QY 541 ILIWDPLNDPAQAEPSPSRRTYYISR 569  
DB 499 ILIWDPLNVSSNGQSDGRSPSRRTYYISR 527  
  
RESULT 14  
Q86SD3 PRELIMINARY; PRT; 621 AA.  
AC Q86SD3;  
DT 01-JUN-2003 (TRENBLrel. 24, Created)  
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)  
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
DE Beta-transducin repeat-containing homologue protein.  
GN Name=C1-betaTSCP;  
OS Ciona intestinalis.
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OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;  
OC Phlebobranchia; Cloniidae; Ciona.  
OX NCBI_TaxID=7719;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hotta K., Takahashi H., Satoh N.;  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: Contains 7 WD repeats.  
DR EMBL; AB076993; BACS7516.1; -.  
DR HSSP; Q9Y297; 1P22.  
DR InterPro; IPR01810; F-box.  
DR InterPro; IPR01680; WD40.  
DR InterPro; IPR01046; WD40_like.  
DR Pfam; PF00646; F-box; 1.  
DR Pfam; PF00400; WD40; 7.  
DR PRINTS; PR00320; GPROTEINRPT.  
DR Prodom; PD000018; WD40; 4.  
DR SMART; SM00256; FBOX; 1.  
DR SMART; SM00320; WD40; 7.  
DR PROSITE; PS50181; FBOX; 1.  
DR PROSITE; PS00678; WD_REPEATS_1; 5.  
DR PROSITE; PS50082; WD_REPEATS_2; 7.  
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.  
KW Repeat; WD repeat.  
SQ SEQUENCE 621 AA; 70791 MW; 6D176B121959F8C3 CRC64;  
  
Query Match 70.1%; Score 2128; DB 2; Length 621;  
Best Local Similarity 72.6%; Pred. No. 1.5e-151;  
Matches 394; Conservative 63; Mismatches 68; Indels 18; Gaps 3;  
  
QY 33 IIPKNSLRQYNSCARLCLNDETVCLASTAMKTEHCVAKTAKLANGTSSMIVPKRK-- 89  
DB 91 ILPSHNIQSL-----QDRIDVRNNTLDSGLPLTNDTVNPAQTVLSPRLRLSQ 140  
  
QY 90 ---LSASYEKEKELCVKYTFEOWSESDOVEFVHILISOMCHYOHGHNSTLYKPMLOQDFIT 146  
DB 141 QLSISENYKNERDSCCTGHPFTWSEQOVDVEFVHILIMCHYOHQINCLFKPMLOQDFIS 200  
  
QY 147 ALPARGLDHAENILSYDAKSLCAELVCCKEMRVVSDGLMKKLIEMRVRTSLMRGL 206  
DB 201 ALPARGLSHAENILSYDAKSLCAELVCCKEMRVVSDGLMKKLIEMRVRTSLMRGL 260  
  
QY 207 AERRGQYLFKNKPPDGNAPNSFYRALYPKIIDIEETIESNNRCGRSLQRIHCRSET 266  
DB 261 SERGMOGHLEFKGRP--NSVPDSFRRSLYPSIISDIEKIESNNRCGRHDLKRLMCSN 318  
  
QY 267 SKGVYCLQYDDOKIYSGLADNTIKIWDKNTLECKRIITGHTGSVLCLODERVIITGSSD 326  
DB 319 SKGVYCLQYDDOKIYSGLADNTIKIWDKNTLECKRIITGHTGSVLCLODERVIITGSSD 378  
  
QY 327 STYRVMDVNTGEMLNTLIHCEAVLHFRNNGMVNTCSKORSIAVWDMASPTDITLRV 386  
DB 379 STYRVMDVNTGEMLNTLIHCEAVLHFRNNGMVNTCSKORSIAVWDMASPTDITLRV 438  
  
QY 387 VGHRAAVNVDPDKXIYASAGDRTIKWNTSTCFYRLTLNGHKGIAICLQYRDRLVSG 446  
DB 439 VGHRAAVNVDPDKXIYASAGDRTIKWNTLTCEFYRLTLNGHKGIAICLQYRDRLVSG 498  
  
QY 447 SSDNTIRLWDIEGACLRVLEGHEELVRCIRFDNKRIYGAAYDGKIKVMDLVAALDPRAP 506  
DB 499 SSDNTIRLWDIEGACLRVLEGHEELVRCIRFDNKRIYGAAYDGKIKVMDLVAALDPRSP 558  
  
QY 507 AGTLCIRTVEHSGRVRLOPDEFQIVSSSHDTIILMDPLNDPAQAEPSPSRRTYY 566  
DB 559 SSTLCIRTVEHSGRVRLOPDEFQIVSSSHDSTILMDPLNDPAQAEPATKSPNRITY 618  
  
QY 567 ISR 569  
DB 619 VQR 621  
  
RESULT 15  
Q44382
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ID 044382 PRELIMINARY; PRT; 510 AA.
AC 044382;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE S11mb.
GN Name=S11mb; Synonyms=s11mb;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98121115; PubMed=9461217; DOI=10.1038/35154;
RA Jiang J., Struhl G.;
RT Regulation of the Hedgehog and Wingless signalling pathways by the F-
box/WD40-repeat protein S11mb.";
RL Nature 391:493-496 (1998).
CC -!- SIMILARITY: Contains 7 WD repeats.
DR EMBL; AF032878; AAC38852.1; -.
DR HSSP; Q9Y297; 1P22.
DR Flybase; FBgn0023423; s11mb.
DR GO; GO:0019005; C:SCF ubiquitin ligase complex; NAS.
DR GO; GO:0045475; P:locomotor rhythm; IMP.
DR GO; GO:0030512; P:negative regulation of transforming growth . . .; NAS.
DR GO; GO:0030178; P:negative regulation of mit receptor signal. . .; NAS.
DR GO; GO:0008590; P:regulation of frizzled signaling pathway; IMP.
DR GO; GO:0030162; P:regulation of proteolysis and peptidolysis; TAS.
DR GO; GO:0008589; P:regulation of smoothened receptor signaling. . .; IMP.
DR GO; GO:0008588; P:release of cytoplasmic sequestered NF-kappaB; IMP.
DR InterPro; IPR001810; F-box.
DR InterPro; IPR001680; WD40.
DR InterPro; IPR011046; WD40_like.
DR Pfam; PF00646; F-box; 1.
DR Pfam; PF00400; WD40; 7.
DR PRINTS; PR00320; GPROTEINBRPT.
DR ProDom; PD000018; WD40; 4.
DR SMART; SM00256; PROX; 1.
DR SMART; SM00320; WD40; 7.
DR PROSITE; PS00678; WD_REPEATS_1; 5.
DR PROSITE; PS50082; WD_REPEATS_2; 7.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
SQ SEQUENCE 510 AA; 58952 MW; DBB0243D3730A5B8 CRC64;

Query Match 68.9%; Score 2089.5; DB 2; Length 510;
Best Local Similarity 78.3%; Pred. No. 9.3e-149;
Matches 394; Conservative 48; Mismatches 54; Indels 7; Gaps 4;

QY 64 MTEHCNCAKTLANG---TSSMIVKQKRLSAS--YEKEKELCVKFFQMSSESDQVEFYE 118
DB 4 METDKIMETN-SNAQAFITTLVDFVRKQSSPTOTERELCFQYFTQMSSEGVDFVE 62
QY 119 HLSQCHYOHGHISYLPMLQRPDFTLPAAGLDHIAENITISYLDASLCAAEIVCKE 178
DB 63 HLLSMCHYOHGHINAYLKPMLQRPDFTLPLKGDHIGENITISYLDASLSSELVCKE 122
QY 179 WYRVTSQGLWKLIERVVRTSDLSWGLAERRGQVLFKNKPPDGNAPPNSFYALYPK 238
DB 123 WLRVISEGLWKLIERKVRTSDLSWGLAERRMMQVLFKPRPQO-TGRPHSFHRELFPK 181
QY 239 ITODIETESNWRGHRSLORHCRSEFSKGYVCLQYDOKTVSGLRDNTIKIMDKNTLE 298
DB 182 IAMDIDSIENNRTRGHRMLRINCSENSKGYVCLQYDQKIVSGLRDNTIKIMDRTDLQ 241
QY 299 CKRIITGHTGSLVCLQYDERVITITGSSDSTVAVMDVNTGEMINTLIHCEAVLHLRFNNG 358
DB 242 CVKTLMGHTGSLVCLQYDQKIVITSSSDSTVAVMDVNTGEMVNTLIHCEAVLHLRFNNG 301
QY 359 MMVTCSKDRSIIVMDMASFTDITLRRVLVGRRAVAVNVDFDDKYIVSASGDRITIKVWNTS 418
DB 302 MMVTCSKDRSIIVMDMTSPSEITLRRVLVGRRAVAVNVDFDEKYIVSASGDRITIKWNTS 361

QY 419 TCEPVRTLNGHKGRIACIQYRDRLVVGSSSDNTIRLMDIEGACLRVLEGHELVRCIRF 478
DB 362 TCEPVRTLNGHKGRIACIQYRDRLVVGSSSDNSITLMDIEGACLRVLEGHELVRCIRF 421
QY 479 DNKRIVSAGAYDGKIKVMDLVVALDPRAPAGTLCRTLVHSGVRRLQFDEFQIVSSSHD 538
DB 422 DTKRIVSAGAYDGKIKVMDLVVALDPRASNTLCNTLVHSGVRRLQFDEFQIVSSSHD 481
QY 539 DTILVDFLNDPAAQAEPPRSPS 561
DB 482 DTILVDFLNDPAAQAEPPRSPS 504

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